

PR 30-JUN-2000; 2000US-0215135.

| Human ovary | AAS24329 | 22 | 470 | 11.6 | 303.2 | 8 |
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PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
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PR 08-DEC-2000; 2000US-0251989.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465570/50.
XX
DR
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX
PS Disclosure; SEQ ID NO 5936; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders, a
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 1462 BP; 409 A; 271 C; 276 G; 506 T; 0 other;
Query Match 55.5%; Score 1449.2; DB 22; Length 1462;

Best Local Similarity 99.58; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1131 TTGCGTATTTGATTTTCATATGCGTTTCTTCTGTAAGTTTTCAGAGATTTTAAA 1190
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Db 1 TTGCGTATTTGATTTTCATATGCGTTTCTTCTGTAAGTTTTCAGAGATTTTAAA 60
QY 1191 TCACAGATCATACTAAATATATTTAGCCTATCAAAAGTTTCCAAAAGCCACACCA 1250
    |||||
Db 61 TCACAGATCATACTAAATATATTTAGCCTATCAAAAGTTTCCAAAAGCCACACCA 120
QY 1251 GTTCGCTACTCAATTTGAAGGGTTTTTACACAGAGGGTGAAGTTAAGTAGAGATTT 1310
    |||||
Db 121 GTTCGCTACTCAATTTGAAGGGTTTTTACACAGAGGGTGAAGTTAAGTAGAGATTT 180
QY 1311 AATTTAAAGCTTAAACCTAGGTAAGAGTAATGAGAAATATTACGGCAATATGCAACTGC 1370
    |||||
Db 181 AATTTAAAGCTTAAACCTAGGTAAGAGTAATGAGAAATATTACGGCAATATGCAACTGC 240
QY 1371 TTGACTGTTTCTTGAGTCTTCTCACTCTAATGTTTAAAGAGGACAAAGAGCTTATG 1430
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QY 1431 GTGCGATTTTCAGTAAACAGGGTGTGTTTGAAGTGCCTTATAGCTCAAGTTCCCTTGT 1490
    |||||
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QY 1491 TCCTAAGTGTGTAATCTGTCTTTAAACGTAAAGAAATGCAAAATATTGAAGTATTTTC 1550
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Db 361 TCCTAAGTGTGTAATCTGTCTTTAAACGTAAAGAAATGCAAAATATTGAAGTATTTTC 420
QY 1551 TGTGTGATGTTTATCTCTCTTCCATTGAGTAATGATGAAATACCTGTGAGAGTAAGAAAT 1610
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QY 1611 GAGTTCTGAGATCTAGTCCCTCTCTGATTCATTAATCTATCCCTTTTCAGTATTA 1670
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QY 1671 CAGTGTCTTAATCTCAGATGTAACCATTTTCACCATGCGAGTGTATCTCATCTCGGCTT 1730
    |||||
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QY 1731 TTCTGGGAATTTGAAGTATCTCTCTTAACCCCAATGTCGAAGGGTGTACTGTATCTTA 1790
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Db 601 TTCTGGGAATTTGAAGTATCTCTCTTAACCCCAATGTCGAAGGGTGTACTGTATCTTA 660
QY 1791 CCACCTTTGAATTTATGAAACGGGTCAATTTACGAAGTCTGCATTTGCTATGAGATATGG 1850
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QY 1851 TTTATAGTACAGCTGAGAGTAAGAACTCAGCGTCCAGATTAACCATGATGCAACCCAGAT 1910
    |||||
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QY 1911 TTTTTCACCTTGATGATACCGTGCATAGGGAATTAAGAGCCGTAATTTTGTCTTATTT 1970
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Db 1021 GGACAGATGATATTCCTCGTGTGTTACTGAAAAACAGGTGTGATCTGTACTGATVACTA 10...
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QY 2511 TGGAAAGCTGTTAAATTAATTTCTCTGTTAAAGGAATTAAGTTTGTCTATTTTGACA 2570
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RESULT 2
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ID AAL01567 standard; cDNA; 779 BP.
XX
AC AAL01567;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen cDNA SEQ ID NO: 1568.
XX
KW Human: reproductive system related antigen; reproductive system disorder;
    cancer; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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PR 14-AUG-2000; 2000US-0225213.

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PR 08-DEC-2000; 2000US-0251989.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX
XX
XX WPI: 2001-465570/50.
DR P-PSDB: AAM95597.
DR
XX
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 1; SEQ ID NO 1568; 1297bp + Sequence Listing; English.
XX
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a coding sequence of the
CC invention.
XX
SQ Sequence 779 BP; 221 A; 130 C; 172 G; 251 T; 5 other;

Query Match 23.2%; Score 606.6; DB 22; Length 779;
Best Local Similarity 95.5%; Pred. No. 5.8e-137;
Matches 677; Conservative 2; Mismatches 21; Indels 9; Gaps 5;

QY 931 GCACACTGCAGCTACAGGCTGATTTTCTGCGCTTTGGAGAACTGATTTAAATACTAGTAG 990
Db 67 GCACAGCAGCTACAGGCTGATTTTCTGCGCTTTGGAGAACTGATTTCAAAATAGTCTAG 126
QY 991 ATTTTCGATAGATCCCATTTTGTACAGAAATTGAATGGATGGATAGGTAAGCAAAA 1050
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| Db | 127 | ATTTCGCAVPAGATGCCATTTTGTGACAGAAATGAATGGATGGAAATGTAACCAAAA | 186 |
| Qy | 1051 | CTAGAACCCCATTTGAGTTTACATTTGATTCACAAATTTGGTTGAGTAGCGTTGGTG | 1110 |
| Db | 187 | GTAAGAACCCCATTTGAGTTTACATTTGATTCACAAATTTGGTTGAGTAGCGTTGGTA | 246 |
| Qy | 1111 | ATAGACTATATTAACCGACGATTTCCGCTATTTTGGATTTTGCATATGAGCGCTTTTTCGTAG | 1170 |
| Db | 247 | ATAGACTATATTAACCGACGATTTCCGCTATTTTGGATTTTGCATATGAGCGCTTTTTCGTAG | 306 |
| Qy | 1171 | TTTTTCAGAGAGATTTTAAATTCACAGAAATCATCTAAATGATATTTTACGCTATCAAACT | 1230 |
| Db | 307 | TTTTTCAGAGAGATTTTAAATTCACAGAAATCATCTAAATGATATTTTACGCTATCAAACT | 366 |
| Qy | 1231 | TCGCAAAAGCCCAACACCCAGCTTCCTGACTCTCAAAATTTGGAAGGGTTTTTGAACAGAGGT | 1290 |
| Db | 367 | TCGCAAAAGCCCAACACCCAGCTTCCTGACTCTCAAAATTTGGAAGGGTTTTTGAACAGAGGT | 426 |
| Qy | 1291 | AGATATTAAGTAGAGTAGATTTAAATTAAGCTTAACCTAGTAGAGTAAGTAATGAGAAATAT | 1350 |
| Db | 427 | AGATATTAAGTAGAGTAGATTTAAATTAAGCTTAACCTAGTAGAGTAAGTAATGAGAAATAT | 486 |
| Qy | 1351 | TACGGCAATATGAGACTGCTTCACTGTTTTCTTGCTGACTCCGCACTCTAAATGTTTTAA | 1410 |
| Db | 487 | TACGGCAATATGAGACTGCTTCACTGTTTTCTTGCTGACTCCGCACTCTAAATGTTTTAA | 546 |
| Qy | 1411 | AGAGCAACAAAGCCTAATGCTGCATATTCAGTAACACAGGGTGGTTTTTAATGCTCTT | 1470 |
| Db | 547 | AGAGCAACAAAGCCTGCTGCTGCATATTCAGTAACACAGGGTGGTTTTTAATGCTCTT | 606 |
| Qy | 1471 | ATAAGCTAGTTTCCCTTGCTTAAAGTGTT-GAATAGCTGCTTTAA--CTAGAAAAAT | 1527 |
| Db | 607 | ATAAGCTAGTTTCCCTTGCTTAAAGTGTTGAATAACCTGCTTTAAAACTAGAAAAAT | 666 |
| Qy | 1528 | GCAAAATATATG--AATGATATTTCTGCTGCTAGTT--PATTCCTGTCATGAGTAGAA- 1583 | |
| Db | 667 | GCAAAATATTTGGAACCTGATATTTTGTGTGTGATTTGATTACTCTTCATTTGAGTGGAA 726 | |
| Qy | 1584 | --TGATGAATACCTGTGAGGATAGAAATGAGTTCTGAGATCTAGTCC 1630 | |
| Db | 727 | TGATGGAATACCTGTGAGGATAGAAATGAGTTCTGAGATCTAGTCC 775 | |
| RESULT 3 | | | |
| AAS94694 | | | |
| ID | AAS94694 | standard; cDNA; 867 bp. | |
| XX | AAS94694: | | |
| AC | | | |
| XX | | | |
| DT | 12-MAR-2002 (first entry) | | |
| XX | | | |
| DE | Rat secreted factor DNA clone p0185_d11. | | |
| XX | | | |
| KW | Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney | | |
| KW | inflammatory disease; congestive heart failure; myocarditis; asthma; ss; | | |
| KW | dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia; | | |
| KW | myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke; | | |
| KW | atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome; | | |
| KW | renal infarction; hereditary nephritis; polycystic kidney disease; | | |
| KW | chronic renal failure; renal vein thrombosis; medullary sponge kidney; | | |
| KW | rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer; | | |
| KW | graft versus host reaction; Crohn's disease; ulcerative colitis; probe; | | |
| XX | Alzheimer's disease; gene therapy. | | |
| OS | Rattus norvegicus. | | |
| XX | | | |
| PN | MO200174901-A2. | | |
| XX | | | |
| PD | 11-OCT-2001. | | |
| XX | | | |
| PE | 23-MAR-2001; 2001MO-US09555. | | |
| XX | | | |
| PR | 31-MAR-2000; 2000US-193548P. | | |

PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234927.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.

PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI: 2001-465570/50.

DR P-PSDB: AAM94290.

XX Isolated nucleic acid molecule encoding a reproductive system antigen -

PT is used in preventing, treating or ameliorating a medical condition -

XX Claim 1; SEQ ID NO 261; 1297pp + Sequence Listing; English.

PS The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a coding sequence of the
CC invention.

XX Sequence 415 BP; 114 A; 79 C; 87 G; 131 T; 4 other;

Query Match 14.8%; Score 386.4; DB 22; Length 415;

Best Local Similarity 97.1%; Pred. No. 9.4e-84; Mismatches 10; Indels 1; Gaps 1;

Matches 401; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 2002 TTTATGTTAATGAGAGATTAGCCCTCCACACAAATGTTCAATTCAGCAAGGCTTCA 2061
DB 1 TTTATGTTAATGAGAGATTAGCCCTCCACACAAATGTTCAATTCAGCAAGGCTTCA 60
QY 2062 TATCCTGTGCTGGGCTGGGATAGAGAGCTTATTCAGGTTTCTGCGCCCTACTATTAC 2121
DB 61 TATCCTGTGCTGGGCTGGGATAGAGAGCTTATTCAGGTTTCTGCGCCCTACTATTAC 120
QY 2122 TCCACTTCACATGCTGGAGACGCGGTAGGAGACATGATTCAATTCGCTGTTACTGAA 2181
DB 121 TCCACTTCACATGCTGGAGACGCGGTAGGAGACATGATTCAATTCGCTGTTACTGAA 180
QY 2182 AAACAGGTGTGATCCTGTTAGTATGATACATAAGTACCTAAATGCTCACTGTTCAATTA 2241
DB 181 AAACAGGTGTGATCCTGTTAGTATGATACATAAGTACCTAAATGCTCACTGTTCAATTA 240
QY 2242 GCAAGTGTTCATACAACTAACTCTTCAATGCTTGGAAAGATATCTACAAAGCAATCT 2301
DB 241 GCAAGTGTTCATACAACTAACTCTTCAATGCTTGGAAAGATATCTACAAAGCAATCT 300
QY 2302 TTATGAATTTGGCCCAAGTAATATCTATGTTTGGCATGGCTATTTAGTACCTCAAA 2361
DB 301 TTATGAATTTGGCCCAAGTAATATCTATGTTTGGCATGGCTATTTAGTACCTCAAA 360
QY 2362 GGTTCACGTGTTTTCGCGGCTGCTCGAGAGTTGTACACACAGTACGCGCAAG 2414
DB 361 GGTTCACGTGTTTTCGCGGCTGCTCGAGAGTTGTACACACAGTACGCGCAAG 412


```
OY 2366 CACGTGTGTTCTGCGCGCTGTCTGAGTTGTCCACCACTGACTGGGCAAGGCTTCTGGGC 2425
|||
DB 225 CACGTGTGTTCTGCGCGCTGTCTGAGTTGTCCACCACTGACTGGGCAAGGCTTCTGGGC 166
|||
OY 2426 ATGATGTAGACAGCTGTGTCTCTTTCCACCTAACAGTTATCTTGACTCTCTGCTGTT 2485
|||
DB 165 ATGATGTAGACAGCTGTGTCTCTTTCCACCTAACAGTTATCTTGACTCTCTGCTGTT 106
|||
OY 2486 ATGCTTACAAATGATGTGCTTATGGAAGGCTGTTAAATATATCTGTTAAAGGA 2545
|||
DB 105 ATGCTTACAAATGATGTGCTTATGGAAGGCTGTTAAATATATCTGTTAAAGGA 46
|||
OY 2546 AATTAAAGTTGTCTATTTTGTACAAATTAACATTTATATTTT 2590
|||
DB 45 AATTAAAGTTGTCTATTTTGTACAAATTAACATTTATATTTT 1
|||

RESULT 8
AAS24329
ID AAS24329 standard; cDNA; 470 BP.
XX
AC AAS24329;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human ovarian PCR-subtracted cDNA library clone #510.
XX
KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
KW primer; probe.
XX
OS Homo sapiens.
XX
PN WO200157207-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03733.
XX
PR 04-FEB-2000; 2000US-0180403.
PR 28-MAR-2000; 2000US-0192745.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Mannion J;
XX
DR WPI: 2001-488879/53.
XX
PT New polynucleotides encoding ovarian tumour proteins, useful for
PT treating ovarian cancer, and as probes, primers, and markers of cancer
PT progression -
XX
PS Example 1; page 194-195; 378pp; English.
XX
CC The invention comprises compositions used for the therapy and diagnosis
CC of ovarian cancer. The compositions comprise one or more ovarian tumour
CC proteins, their associated polynucleotides, or immunogenic portions of
CC the proteins. The ovarian tumour polynucleotides and polypeptides are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein. They are also useful for inhibiting the development of cancer in
CC a patient with an ovarian tumour DNA or protein by incubating isolated
CC T-cells allowing them to proliferate, and administering to the patient.
CC The sequences can be used as markers for cancer, for example, to monitor
CC ovarian cancer progression. Probes and primers are useful in nucleic acid
CC hybridisation, in detecting the presence of complementary sequences in a
CC given sample, for preparing mutant species and for preparing other
CC genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
CC represent human ovarian tumour protein cDNA clones.
XX
SQ Sequence 470 BP; 119 A; 98 C; 96 G; 151 T; 6 other;
```

```
Best Local Similarity 97.9%; Pred. No. 1,4e-63;
Matches 327; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
OY 1992 CCGATTTTGTGCTTATTTCCAACTAAGTAGTCAATATCTCTTCTTTTATGTTAA 2011
|||
DB 2 CCGATTTTGTGCTTATTTCCAACTAAGTAGTCAATATCTCTTCTTTTATGTTAA 61
|||
OY 2012 TGAGAAATTTAGCTCCACCTCCACATTCATTCATTTGAGCAAGGCTTTCATATCCCTGCT 2071
|||
DB 62 TGAGAAATTTAGCTCCACCTCCACATTCATTCATTTGAGCAAGGCTTTCATATCCCTGCT 121
|||
OY 2072 GTGGTCTGTGATTAAGAGAGCTTATTCAGGTTCCGCCCTAGCTTTAGCTTCATTCAC 2131
|||
DB 122 GTGGTCTGTGATTAAGAGAGCTTATTCAGGTTCCGCCCTAGCTTTAGCTTCATTCAC 181
|||
OY 2132 ATGCTGGAGACCTGGGCTAGGAGACAGATGATTCATCTGTGTTACTGAAAAACAGGTGT 2191
|||
DB 182 ATGCTGGAGACCGGCGGTAGGAGACAGATGATTCATCTGTGAGTTACTGAAAAACAGGTGT 241
|||
OY 2192 GATTCCTGTAGTACTATTAAGTACCTTAAATGTCACTGTTCAATTTAGCAAGTGTTC 2251
|||
DB 242 GATTCCTGTAGTACTATTAAGTACCTTAAATGTCACTGTTCAATTTAGCAAGTGTTC 299
|||
OY 2252 TAACAACCTAAACTCTTCAATGCTTGGAAAGAT 2285
|||
DB 300 TAACAACCTAAACTCTTCAATGCTTGGAAAGAT 333
|||

RESULT 9
AAH82918
ID AAH82918 standard; cDNA; 470 BP.
XX
AC AAH82918;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:542.
XX
KW Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
KW immunogenic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200151513-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01575.
XX
PR 14-JAN-2000; 2000US-0176722.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA;
XX
DR WPI: 2001-425866/45.
XX
PT Novel ovarian tumor proteins, and nucleic acids encoding them, used to
PT treat and diagnose cancers, particularly ovarian cancer -
XX
PS Claim 5; Page 164; 338pp; English.
XX
CC AAH82377 to AAH83878 represent human ovarian tumour-associated
CC polynucleotide sequences which encode ovarian tumour proteins. The
CC ovarian tumour protein and polynucleotide sequences have cytostatic
CC activity, and can be used in gene therapy and vaccine production. The
CC ovarian tumour proteins and polynucleotides can be used to inhibit
CC the development of cancer, particularly ovarian cancer. They can also
CC be used to diagnose the onset and progression of cancer.
XX
SQ Sequence 470 BP; 119 A; 98 C; 96 G; 151 T; 6 other;
```

Query Match 11.6%; Score 303.2; DB 22; Length 470;

Best Local Similarity 97.98; Pred. No. 1,4e-63;
Matches 327; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1952 CCGATTTTGTCTTATTCACACTAGTAGATCATCTCTTCTTTTATGTTAA 2011
|||
Db 2 CCGATTTTGTCTTATTCACACTAGTAGATCATCTCTTCTTTTATGTTAA 61
|||
QY 2012 TCGAGAAATTTAGCCCTCCACTCAACAATGTTCAAATTCAGCAAGGCTTTCATATCTTGGCT 2071
|||
Db 62 TCGAGAAATTTAGCCCTCCACTCAACAATGTTCATTCAGCAAGGCTTTCATATCTTGGCT 121
|||
QY 2072 GTGGGTGGATGATGAGGCTTATTCAGTTCCTGGCTTACGCTTACACTTCCACTTAC 2131
|||
Db 122 GTGGGTGGATGATGAGGCTTATTCAGTTCCTGGCTTACGCTTACACTTCCACTTAC 181
|||
QY 2132 ATGCTGGAGACGGCGCTAGGAGACAGATGTATTCCTGGTGTACTGAATAACAGGTGT 2191
|||
Db 182 ATGCTGGAGACGGCGCTAGGAGACAGATGTATTCCTGGTGTACTGAATAACAGGTGT 241
|||
QY 2192 GATCCTGTAGTGATCTATATAGTACCTAAATGTCACTGTTCAAATTCAGCAAGTGTTC 2251
|||
Db 242 GATCCTGTAGTGATCTATATAGTACCTAAATGTCACTGTTCAAATTCAGCAAGTGTTC 299
|||
QY 2252 TAACCAACTAAACTCTCAATGCTTGAAGAAT 2285
|||
Db 300 TAACCAACTAAACTCTCAATGCTTGAAGAAT 333
|||

RESULT 10
AAL35611
ID AAL35611 standard; cDNA; 244 BP.
XX
AC AAL35611;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 953.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antifungal;
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KM neurological disease; infection; human; secreted protein;
musculoskeletal system; ss.
XX
OS Homo sapiens.
XX
PN WO200155367-A1.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01338.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216860.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233053.
PR 14-SEP-2000; 2000US-0233054.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.

XX Sequence 212 BP; 50 A; 49 C; 62 G; 51 T; 0 other;
 SQ
 Query Match 6.3%; Score 164.8; DB 21; Length 212;
 Best Local Similarity 89.0%; Pred. No. 3.2e-30;
 Matches 178; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 OY 179 CGCGAAGAAACAGAGCCGTTGACCATGTTGCAACTGGCAGTTTGAGCAAGCAAGACC 238
 13 CGCGAGGAAACAGAGCCGTTGACCATGTTGCAAGCGGAGTTGAGCAAGCAAGACC 72
 Db
 OY 239 GGGCAGATTTCAGAAATGCTGACATGCTATCACCAGACAGCCCTGCTAACTGATTT 298
 73 GGGCAGATTTCAGAAATGCTGACATGCTATCACCAGACAGCCCTGCTAACTGATTT 132
 Db
 OY 299 TGACTACTGGATTATGTTGTTCCCTGAACCAACCTCAACGAGGTAAATATTGAGGATC 358
 133 CGACTACTGGATTATGTTGTTCCCTGAACCAACCTCAACGAGGTAAATATTGAGGATC 192
 Db
 OY 359 AACTTGCCAGAAATTTGGTTA 378
 193 AACATGCCAGAAATTTGGTTA 212
 Db
 RESULT 12
 AAC32046
 ID AAC32046 standard; cDNA; 133 BP.
 AC AAC32046;
 XX
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein 5' EST, SEQ ID NO: 36121.
 XX
 KM Human: 5' EST: expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 9905-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 XX
 PS
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX
 XX Claim 1: SEQ ID 36121; 71pp + CD-ROM; English.
 PS
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC cDNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNA or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

XX Sequence 133 BP; 40 A; 18 C; 28 G; 41 T; 6 other;
 SQ
 Query Match 4.2%; Score 109.8; DB 21; Length 133;
 Best Local Similarity 95.2%; Pred. No. 5.3e-17;
 Matches 119; Conservative 4; Mismatches 1; Indels 1; Gaps 1;
 OY 1004 ATCCCATTTTGTACAGAAATG-AATGGATGCAATGATGAACCAAGTAAGACCCAT 1062
 9 ATCCCATTTTGTACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 68
 Db
 OY 1063 TTGAGTTTACATTGATTCACCAATTTGTTTACGATGAGCTTGATGATGATGATGAT 1122
 69 TTGAGTTTACATTGATTCACCAATTTGTTTACGAGAGGCTTGATGATGATGATGATGAT 128
 Db
 OY 1123 AACCA 1127
 129 AACCA 133
 Db
 RESULT 13
 AA241261
 ID AA241261 standard; cDNA; 1491 BP.
 AC AA241261;
 XX
 DT 18-JAN-2000 (first entry)
 DE Human normal ovarian tissue derived cDNA 40.
 XX
 KM Human: ovary; screening; ovarian cancer; treatment; ss.
 KM
 OS Homo sapiens.
 XX
 PN DE19816395-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 03-APR-1998; 98DE-1016395.
 XX
 PR 03-APR-1998; 98DE-1016395.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dall E;
 XX
 DR WPI; 1999-552352/47.
 XX
 DR P-PSDB; AAY59820, AAY59821, AAY59822.
 XX
 PT Nucleic acid sequences potentially useful in diagnosis or therapy of
 PT ovarian cancer -
 XX
 PS
 PT Claim 3: Page 153; 274ppp; German.
 XX
 CC This invention describes novel nucleic acid sequences that are highly
 CC expressed in normal ovarian tissue. Artificial chromosomes and cosmid
 CC clones containing the sequences can be used as gene transfer vehicles.
 CC The sequences can be used to produce DNA fragments containing
 CC full-length genes. Host cells transformed with the sequences can be used
 CC to produce polypeptides or polypeptide fragments, which can be used to
 CC screen phage displays for polypeptides that bind to them, or as tools for
 CC identifying agents active against ovarian cancer, or to prepare
 CC medicaments for treating ovarian cancer. The cDNA sequences can be used
 CC to obtain genomic genes, their promoters, enhancers, silencers, exon
 CC structures, intron structures and their splice variants. AA241222-241324
 CC represent cDNA sequences derived from normal human ovarian tissue and
 CC which encode the protein fragments represented in AAY59724-Y59837.
 XX
 SQ Sequence 1491 BP; 323 A; 362 C; 455 G; 351 T; 0 other;
 Query Match 2.6%; Score 67.2; DB 20; Length 1491;
 Best Local Similarity 51.2%; Pred. No. 3e-06;
 Matches 206; Conservative 0; Mismatches 193; Indels 3; Gaps 2;

PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 9905-0127607.
PR 02-APR-1999; 9905-0127636.
PR 05-APR-1999; 9905-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkels RA, Leach M;
XX
DR MPI; 2000-602362/57.
P-PSDB; AAB43235.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 5; Page 5174-5176; 5507pp; English.

CC AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;
CC osteoparitic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;
CC antihypertoid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy.
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

CC
SQ Sequence 1759 BP; 392 A; 548 C; 463 G; 356 T; 0 other;

Query Match 2.6%; Score 67.2; DB 21; Length 1759;
Best Local Similarity 51.2%; Pred. No. 3.3e-06;

Matches 206; Conservative 0; Mismatches 193; Indels 3; Gaps 2;

OY 351 GAGGAATCAACTGCCAATTTGGTTAAATGCTGAGAACTGTCGCCAATCAAG 410
DB 1297 GATGAACACTTGTGTGCAACCTGATGCACTCTGCGAGAGACCTGGCCAGGCCGG 1238
OY 411 CAAACTAACTTGGTCTCAAGGTCCTTGTCTCCAGAACTGACGCAAGAAATTCCT 470
DB 1237 CTGGGCTTCGACGCCCTGGCGCCCTGATGCTAGCCAGTTGGTAACCAAGTGGGC 1178
OY 471 CAAGATGTCCTGGGCTTTCCTCAACGAGACCTGGGCTTGGAGCTTGTATGAC 530
DB 1177 AAGAAGTACTGCGCTGCTACAGGAGCCGTCGGCTCGGGGGGCGCTGCTGAC 1118
OY 531 GTGAACCTGGAATTAATAATGTATGTAATAAACCTGATAGATTGTGTGATTTAGC 590
DB 1117 GTCTGGTGGAGGAGGCAAGAGCTGCCACAGGCTGGCCAGCTGCACCTGACCCAGC 1058
OY 591 GTGTACCTACTTTTGAAGCTTACACTTGTGTTAAGCAGA-GAAGCTGATGAGTAG 649
DB 1057 CTGGTGGCCACCTTCACAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 998
OY 650 CTTGAGGAGCTTTT--CTTTAGTAGAGTGGTCTCTCTGCTTCTGCTTCAAGAGACTG 707
DB 997 ATCCAGAGGCTGTTTACGCTCGCAACTCTCCCTTCCTGCTTCAAGCAGTCCCTG 938
OY 708 ATCCTCAGCTCAGGATTTGACTGTTAAGAAAAAATTTC 749

DB 937 ACGCTGAGCACTGGCTTCGAGTCAATCAAGAAAGCTGTAC 896
Search completed: October 13, 2002, 03:59:24
Job time : 423 secs


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,814
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/684,101
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UPXD:503/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: na
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1677 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 313..727
US-09-205-814-1

Query Match 1.9%; Score 50.8; DB 4; Length 1677;
Best Local Similarity 61.2%; Pred. No. 0.0003;
Matches 82; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 2477 TTGCCTGTATGCTTACAAATGCTGATGCTTATGGAAGCTGTTAAATTAATTCCT 2536
Db 1542 TTCAATTTTGGCATTTGCAAAATTAACAAGAAATATTGAAATTAATCAGTAAGATGCA 1601
QY 2537 GTTAAGGAATTTAAAGTCTGCTATTGTCATATTTTGACATATAACATTATATTATTTAAAAA 2596
Db 1602 TTGTAGAAATTTAAATTTTATTATAGACACAACAGCAAAATAATTAATCTTTTATATAA 1661
QY 2597 AAAAAAAAAAAAAA 2610
Db 1662 AAAAAAAAAAAAAA 1675

RESULT 4
US-08-642-274D-17/c
Sequence 17, Application US/08642274D
Patent No. 6200749
GENERAL INFORMATION:
APPLICANT: Shlöh, Josef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
FILE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 220
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 448
TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genomic
US-08-642-274D-17

```

| | | | | |
|-----------------------|-----------------|------------------|-----------|-------------|
| Query Match | 1.68; | Score 41; | DB 4; | Length 448; |
| Best Local Similarity | 57.48; | Pred. No. 0.073; | | |
| Matches 74; | Conservative 0; | Mismatches 55; | Indels 0; | Gaps 0; |

| | | | | |
|----|------|---|--------------------------------|------|
| Qy | 1159 | TTTTTCGTGAAGTTTTCAGAGGATTTT | TTTAAATCAGAGATATCTAATCATATTTTG | 1218 |
| | | | | |
| Db | 313 | TATTTCTGATAGTTTGAAGAATAGTTCATGTACAGAGTCATTTTATAGCCTTTTGT | | 254 |
| Qy | 1219 | CCCTTCAAACTTCCAAAAGCCACACACCAATTCCTGATCAATTTTGAGGGTTTT | | 1278 |
| | | | | |
| Db | 253 | GAGAACACAGTTTAAAAAGCCCAATGCCAGTTTAAAAAATAATTTACAGAGAAATTT | | 194 |
| Qy | 1279 | AGACAGAG | 1287 | |
| | | | | |
| Db | 193 | CTAATGTG | 185 | |

RESULT 5
US-08-952-014C-17/c
; Sequence 17, Application US/08952014C
; Patent No. 6265158

```

: GENERAL INFORMATION:
: APPLICANT: Shihob, Yosef
: TITLE OF INVENTION: ATAXIA-TELANGELECTASIA GENE AND ITS
: TITLE OF INVENTION: GENOMIC ORGANIZATION
: NUMBER OF SEQUENCES: 91
: CORRESPONDENCE ADDRESS:

```

STREET: 30500 No. 626516thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

```

1  FILING DATE:
2  CLASSIFICATION:
3  ATTORNEY/AGENT INFORMATION:
4  NAME:  kohn, kenneth I.
5  REGISTRATION NUMBER:  30,995
6  REFERENCE/DOCKET NUMBER:  2290.00028
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE:  810-539-5050
9  TELEFAX:  810-539-5055
10 INFORMATION FOR SEQ ID NO:  17:
11
12 SEQUENCE CHARACTERISTICS:
13     LENGTH:  448 base pairs
14     TYPE:  nucleic acid
15     STRANDEDNESS:  single
16     TOPOLOGY:  linear
17 MOLECULE TYPE:  DNA (genomic)
18
19 US-08-952-014C-17

```

```

Query Match      1.6%; Score 41; DB 4; Length 418;
Best Local Similarity 57.4%; Pred. No. 0.073;
Matches 74; Conservative 0; Mismatches 55; Indels 0; Gaps
0Y 1159 TTTTTCGTAGTTTCAGAGGATTTTTTAAATCAGAGATCATACTAAATGATTTAG 1218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 313 TATTTTCGATGATTTTGAAGCAATAGTCGATCATACAGAGCATTTTATAGGCTTTTGT 254
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 1219 CCTATCAAAACTTCGAAAACCCACACACACATCTCCTGACATCAATTTGAAGGCTTTT 1278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

| | | | |
|----|------|---|------|
| Db | 253 | GAGAAACACAGGTTTTAAAGGCCCAATGCCAGCTTTAAAAAAAATTTAACGAGAAATTT | 194 |
| Qy | 1279 | AGACACGAG | 1287 |
| Db | 193 | CTAAATCTG | 185 |

US-09-293-322C-8
; Sequence 8, Application US/09293322C

```

: Patent No.6232110
: GENERAL INFORMATION:
: APPLICANT: Pallas, David C
: APPLICANT: Du, Xianxing
: TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methyltransferase
: Patent No.6232110
: TITLE OF INVENTION: Recombinant DNA Molecules and Methods

```

```

1 CURRENT APPLICATION NUMBER: US/09/293,322
2
3 CURRENT FILING DATE: 1999-04-16
4
5 PRIOR APPLICATION NUMBER: US 60/082,202
6
7 PRIOR FILING DATE: 1998-04-17
8
9 NUMBER OF SEQ ID NOS: 17
10
11 SOFTWARE: PatentIn Ver. 2.0
12
13 SEQ ID NO 8
14
15 LENGTH: 2409
16
17 TYPE: DNA
18
19 ORGANISM: Mus musculus
20
21 FEATURE:
22
23 NAME/KEY: misc_feature
24
25 LOCATION: (1)..(2409)
26
27 OTHER INFORMATION: N is A, T, G or C.
28
29 US-09-293-322C-8

```

| | | | | |
|-----------------------|-----------------|-----------------|-----------|--------------|
| Query Match | 1.68; | Score 41; | DB 4; | Length 2409; |
| Best Local Similarity | 56.28; | Pred. No. 0.18; | | |
| Matches 77; | Conservative 0; | Mismatches 60; | Indels 0; | Gaps 0 |

| | | | |
|----|------|---|------|
| QY | 2474 | CTCTGGCTGTTATGCTTAACAAAATGTAATGGCTATGGAAGGCTGTAATTAATTT | 2533 |
| | | | |
| Db | 2257 | CTGTGCTCCTGCTGCACGTCACAGTCGTGGAGCCGACTTTGTTCTTTATTTATGAT | 2316 |
| QY | 2554 | CCCTTTAAAGCAATTTAACTGTTGCTATTTTGGACAATTAACATTAATATTTTAAAA | 2592 |
| | | | |
| Db | 2317 | CTTGTGTTAAAGCAATTAATATATCTCCACACTTTAAAAAATAAAAAAAAAAAAAA | 2376 |
| QY | 2594 | AAAAAAAAAAAAAAAAAAAA 2610 | |
| | | | |
| Db | 2377 | AAAAAAAAAAAAAAAAAAAA 2393 | |

RESULT 7
 US-09-004-731-40
 : Sequence 40, Application US/09004731
 : Patent No. 6177258
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Wu Hunter, Shirley
 :
 : APPLICANT: Stiegler, Gary
 :
 : APPLICANT: Gaines, Patrick J.
 :
 : TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
 :
 : TITLE OF INVENTION: MOLECULES AND USES THEREOF
 :
 : NUMBER OF SEQUENCES: 103

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;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;

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```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,731
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,699
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..728
FEATURE:
NAME/KEY: Xaa = any amino acid
LOCATION: 62
FEATURE:
NAME/KEY: Xaa = any amino acid
LOCATION: 209
US-09-004-731-40

```

```

Query Match          1.5%; Score 39.6; DB 4; Length 841;
Best Local Similarity 67.5%; Pred. No. 0.25;
Matches    54; Conservative   0; Mismatches    26; Indels     0; Gaps      0;

QY   2531 ATTCCTGTTAAAGGAATTAAGTTTGTCTATTATTTTGACAATAAACAATATATATTTT 2590
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    755 AGTTGATATAACCTNCACTGCATGAATTTGTTTATTATTGGAAATAAATATATTTNTGAAA 814
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY   2591 AAAAAAAAAAAAAAAAAAAAAA 2610
      ||||||| ||||||| |||||
Db    815 AAAAAAAAAAAAAAAAAAAAAA 834

RESULT 8
US-09-004-731-42/c
: Sequence 42, Application US/09004731
: Patent No. 6177258
: GENERAL INFORMATION:
  APPLICANT: Wu Hunter, Shirley
  APPLICANT: Stiegler, Gary
  APPLICANT: Gaines, Patrick J.
  TITLE OF INVENTION: PLEA PROTEASE PROTEINS, NUCLEIC ACID
  TITLE OF INVENTION: MOLECULES AND USES THEREOF
  NUMBER OF SEQUENCES: 103
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sheridan Ross P.C.
    STREET: 1700 Lincoln Street, Suite 3500
    CITY: Denver
    STATE: Colorado
    COUNTRY: USA
    ZIP: 80203
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentln Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/004,731
    FILING DATE:
    CLASSIFICATION:

```

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US/08/749,699
3 FILING DATE:
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Connell, Gary J
6 REGISTRATION NUMBER: 32,020
7 REFERENCE/DOCKET NUMBER: 2618-25-C3
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (303) 863-9700
10 TELEFAX: (303) 863-0223
11 INFORMATION FOR SEQ ID NO: 42:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 841 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: DNA (genomic)
18
19
20 US-09-004-731-42

```

```

Query Match 1.5%; Score 39.6; DB 4; Length 841;
Best Local Similarity 67.5%; Pred. No. 0.25;
Matches 54; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2531 ATTCCTGTTAAAGAAATTAAGTTGTCTATTTTGGACAATAAATCATTAATATTTT 2590
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 87 AGTTGTAATAACCTNCCATGGAATGTGTTTATTTTGGAAATAAATATTAATTTTGGAA 28
      |||||
QY 2591 AAAAAAAAAAAAAAAAAA 2610
      |||||
Db 27 AAAAAAAAAAAAAAAAAA 8

RESULT 9
US-09-032-215-46
; Sequence 46, Application US/09032215
; Patent No. 6204010
; GENERAL INFORMATION:
; APPLICANT: Stiegler, Gary L.
; APPLICANT: Gaines, Patrick J.
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII DOS TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,215
; FILING DATE: 27-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 841 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single

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US-09-032-215-48

QY 2531 ATTTCCTGTTAAAGGAATTTAAAGTTTTGTCATATTTTTGACCAATTAAAACATTATATATTTTTT 25900

Db 755 AGTTGTATAAACCCTNCCAATGAAATGGTTTATATTTTGGAAATTAATAATATTTTNGAAA 814

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10087
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,066
FILING DATE: 20-NOVEMBER-1991
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-028PC
TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
CELL TYPE: T-cell blast
IMMEDIATE SOURCE:
LIBRARY:
CLONE: BD4-T3
PCT-US92-10087-16

Query Match 1.5%; Score 39.4; DB 5; Length 198;
Best Local Similarity 56.6%; Pred. No. 0.13; Mismatches 56; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
Qy 2482 TGTATGCTTACAAATGCTGATGCTATGGAAGCTGTTAAATTAATTAATTCCTGTTAA 2541
Db 70 TATTTTGTATTAAGTCCTTCCTTATTTGTAAGCTGTTAATTAATTAATTAATTAATTA 129
Qy 2542 AGCAATTAAGTTGCTATTTTGCACATTAACATTAATTAATTTTAAATTAATTAATTA 2601
Db 130 ATATATTAAAGCAAAATGTTCAAGAAAAAATTAATTAATTAATTAATTAATTAATTA 189
Qy 2602 AAAAAAAA 2610
Db 190 AAAAAAAA 198

RESULT 15
US-08-441-139-8
Sequence 8, Application US/08441139
Patent No. 573245
GENERAL INFORMATION:
APPLICANT: Wiltup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6030 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1004..4753
US-08-441-139-8

Query Match 1.5%; Score 39.4; DB 1; Length 6030;
Best Local Similarity 51.4%; Pred. No. 0.84; Mismatches 86; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
Qy 2433 TAGACGTGTGCTTCCCACTAACAGTATCTTGACCTGCTGCTGATGCTTA 2492
Db 4810 TTGCATTTGCTTCACCCCTCAGTATCCCTTGTGTTTATTTCTCGGAACATTA 4869
Qy 2493 CAAATGCTGATGCTTATGGAAGCTGTTAAATTAATTAATTCCTGTTAAAGAAATTA 2552
Db 4870 ACACTGCATGAATTTGTACTTCTCTTTAATCCAGTCCGGTAAGCATCATCA 4929
Qy 2553 GTTGTCTATTTTACACATTAACATTAATTAATTTTAAATTAATTAATTAATTA 2609
Db 4930 ATTTTATTCGACCTCGTTAAGTCATTAATTTTTCCTCCAAATTAACATAACAA 4986

Search completed: October 13, 2002, 04:01:03
Job time : 98 secs

| | | | | | |
|------------|-------|-------|-------|-------|----------|
| BASE COUNT | 309 a | 196 c | 224 g | 335 t | 2 others |
|------------|-------|-------|-------|-------|----------|

QY 457 CGCAGAAATTTGCTCAGATGTCTCGCGCTTTCCTCAGAGGAGCCCTGCGCTTCGAG 516
 1 |||||||
 Db 244 CCCAGAGAAATGCTCAAGATGTCTCGCGCTTTCCTCAGAGGAGCCCTGCGCTTCGAG 303
 517 GTTGTGTTATGCTCAGTGAATTTGGAATATGATGTAATAAGCTGATGATTTG 576
 |||||||
 Db 304 GTTGTGTTATGCTCAGTGAATTTGGAATATGATGTAATAAGCTGATGATTTG 363
 577 TGTGTGATTTAGCGGTGCTACCTACTTTTGAAGCTTACCTGTTTAAGCAGAGAAT 636
 |||||||
 Db 364 TGTGTGATTTAGCGGTGCTACCTACTTTTGAAGCTTACCTGTTTAAGCAGAGAAT 423
 637 GCTATGAGCTAGCTTACGAGACTTTTCTTATGAGAGTGGCTTCTCTGCTGTTCA 696
 |||||||
 Db 424 GCTATGAGCTAGCTTACGAGACTTTTCTTATGAGAGTGGCTTCTCTGCTGTTCA 483
 697 GGAGAACTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756
 |||||||
 Db 484 GGAGAACTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
 757 TTGGAACACAGTATGTAAGGGTCTTAAAGGAAATATATTAAGATTTATTCATGA 816
 |||||||
 Db 544 TTGGAACACAGTATGTAAGGGTCTTAAAGGAAATATATTAAGATTTATTCATGA 603
 817 TTGGGTGTAATGATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
 |||||||
 Db 604 TTGGGTGTAATGATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
 877 CTAAATTAAGAAACCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
 |||||||
 Db 664 CTAAATTAAGAAACCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 936 TGCAGCTAACGCGCTGATTTT 956
 |||||||
 Db 724 TGCAGCTAACGCGCTGATTTT 744

RESULT 3
 Bf971140 931 bp mRNA linear EST 22-JAN-2001
 LOCUS 602270723F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4358981 5',
 mRNA sequence.
 ACCESSION Bf971140
 VERSION Bf971140.1 GI:12338355
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 931)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apds@email.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM997 row: n column: 06
 High quality sequence stop: 663.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4358981"
 /clone_lib="NIH_MGC_84"
 /tissue_type="adrenal cortex carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: adrenal gland; Vector: pCMV-Sport6; Site_1:"

Query Match 25.4%; Score 662.8; DB 10; Length 931;
 Best Local Similarity 99.6%; Pred. No. 1.6e-106;
 Matches 664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Note: this is a NIH_MGC Library."

BASE COUNT 233 a 202 c 216 g 279 t 1 others

ORIGIN

QY 302 CTACTGGGATTTATGTTTCTTCCCTGAGACCCACCTCAGCAGAGTAATTTGAGATCAAC 361
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 Db 1 CTACTGGGATTTATGTTTCTTCCCTGAGACCCACCTCAGCAGAGTAATTTGAGATCAAC 60
 362 TTGCAGAAATTTGGTTAAATGCTGGAACAGCTGCTGCTCAAAATCAAGCAAACTAACT 421
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 Db 61 TTGCAGAAATTTGGTTAAATGCTGGAACAGCTGCTGCTCAAAATCAAGCAAACTAACT 120
 422 TGGTTGCTCAAGGCTCTTGTCCCTGAGAACTGACGAGAAATTTGCTCAAGATGCTCT 481
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 Db 121 TGGTTGCTCAAGGCTCTTGTCCCTGAGAACTGACGAGAAATTTGCTCAAGATGCTCT 180
 482 GCGGCTTCTCCACAGGAGCCCTGGGCTGGGAGGTTGTTATGACAGTGAACCTTGA 541
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 Db 181 GCGGCTTCTCCACAGGAGCCCTGGGCTGGGAGGTTGTTATGACAGTGAACCTTGA 240
 542 AATTGAAATGATGTAATAAGCTGATGAGATTTGCTGCTGCTTACCGTCTACCTAC 601
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 Db 241 AATTGAAATGATGTAATAAGCTGATGAGATTTGCTGCTGCTTACCGTCTACCTAC 300
 602 TTTTGTGCTTACACTTGTGTTTAAGCAGAGAACTGCTCATGAGTACCTTCAGGACTT 661
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 Db 301 TTTTGTGCTTACACTTGTGTTTAAGCAGAGAACTGCTCATGAGTACCTTCAGGACTT 360
 662 TTTCTTTAGTAGAGGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
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 Db 361 TTTCTTTAGTAGAGGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 722 ATTTCGACTTGTAAAGAAACCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
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 Db 421 ATTTCGACTTGTGTAAAGAAACCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 782 CTAAAGAGGAAATATTAAGATTAATGATTTGATGTTGGTATTAACCTATTCAGCTAG 841
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 Db 481 CTAAAGAGGAAATATTAAGATTAATGATTTGATGTTGGTATTAACCTATTCAGCTAG 540
 842 TCAGCTAAGTCATTTGTAGTTTGGCCACCTGCTTAAATTAAGAAACCCCAATGTAGT 901
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 Db 541 TCAGCTAAGTCATTTGTAGTTTGGCCACCTGCTTAAATTAAGAAACCCCAATGTAGT 600
 902 CTCTTTCTTCTGCTGCTTACATTCATAGCAACTGACGCTAACGCGCTGATTTTCTGCG 961
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 Db 601 CTCTTTCTTCTGCTGCTTACATTCATAGCAACTGACGCTAACGCGCTGATTTTCTGCG 660
 962 CTTTGGGA 968
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 Db 661 CTTTGGGA 667

RESULT 4
 Bf790530 723 bp mRNA linear EST 12-JAN-2001
 LOCUS 602250214F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4337787 5',
 mRNA sequence.
 ACCESSION Bf790530
 VERSION Bf790530.1 GI:12095584
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 723)

QY 411 CAAACTAACTGTGTGCTCAAGGCTCTTCCCTGAGAACTGACGAGAAATTGCT 470
DB 121 CAACTAACTGTGTGCTCAAGGCTCTTCCCTGAGAACTGACGAGAAATTGCT 180
QY 471 CAAGATGCTGCGGCTTCTCTCAAGGAGCCCTGCGGCTGCGAGGTTGTTATGAC 530
DB 181 CAAGATGCTGCGGCTTCTCTCAAGGAGCCCTGCGGCTGCGAGGTTGTTATGAC 240
QY 531 GTGAAGTTGGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 590
DB 241 GTGAAGTTGGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 300
QY 591 GTGCTACTACTTTTGAAGCTTACCTGTGTTTGAAGGAGAACTGCTGACATGAC 650
DB 301 GTGCTACTACTTTTGAAGCTTACCTGTGTTTGAAGGAGAACTGCTGACATGAC 360
QY 651 TTGAGGAGCTTTTCTTGAAGAGTGCCTTCTCTGTTTCAAGGAGAACTGCTGATC 710
DB 361 TTGAGGAGCTTTTCTTGAAGAGTGCCTTCTCTGTTTCAAGGAGAACTGCTGATC 420
QY 711 CTGAGCTGAGATTTGCACTTTGTTAAGAAAAAATTACTGATTTGAACAACAGT 770
DB 421 CTGAGCTGAGATTTGCACTTTGTTAAGAAAAAATTACTGATTTGAACAACAGT 480
QY 771 ATTGAAGGCTCTTGAAGGAGAAATATATTAAGATTTTCAATGATTTGATTAAC 830
DB 481 ATTGAAGGCTCTTGAAGGAGAAATATATTAAGATTTTCAATGATTTGATTAAC 540
QY 831 TATTCAGCTAGTCACTTAAGTCAATTTGATTTGCCCCACCTGCTTAATTAAGAAC 890
DB 541 TATTCAGCTAGTCACTTAAGTCAATTTGATTTGCCCCACCTGCTTAATTAAGAAC 599
QY 891 CCAATATGATCTTTTCTTCTTCTGTTTGTGTTTGTACATTATACAACTGCAAGAGCT 950
DB 600 CCAATATGATCTTTTCTTCTTCTGTTTGTGTTTGTACATTATACAACTGCAAGAGCT 658
QY 951 GATTTTCTGCGCTTTGAGAGATGATTCAAATATGATTTGATTTGCAATGATTTCCAT 1010
DB 659 GATTTTCTGCGCTTTGAGAGATGATTCAAATATGATTTGATTTGCAATGATTTCCAT 715
QY 1011 TTTTGTACAGAAATTGA 1026
DB 716 TTTTGTACAGAAATTGA 731

RESULT 6
BE886599 763 bp mRNA linear EST 20-OCT-2000
LOCUS 601509345F1 NIH_MGC_71 Homo sapiens cdna clone IMAGE:3910762 5',
DEFINITION mRNA sequence.
ACCESSION BE886599
VERSION BE886599.1 GI:10341048
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 763)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM726 row: j column: 11
High quality sequence stop: 701.

FEATURES
Source Location/Qualifiers
1..763
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3910762"
/clone_lib="NIH-MGC_71"
/tissue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 181 a 183 c 201 g 197 t 1 others
ORIGIN
Query Match 24.8% Score 647; DB 10; Length 763;
Best Local Similarity 96.1% Pred. No. 1e-103;
Matches 697; Conservative 0; Mismatches 20; Indels 8; Gaps 3;
QY 41 GCTGCTCTGCGGCTCTGAGTCAAGGCTCTTCCCTGAGAACTGACGAGAAATTGCT 100
DB 1 GCTGCTCTGCGGCTCTGAGTCAAGGCTCTTCCCTGAGAACTGACGAGAAATTGCT 60
QY 101 CCTGCTCTGTTTACCCGCGAGAGCGGAGGCGCCCGGAACTCTGCGAGCGCTCA 160
DB 61 CCTGCTCTGTTTACCCGCGAGAGCGGAGGCGCCCGGAACTCTGCGAGCGCTCA 120
QY 161 GGAAGGCGCTTCCGCTCGCGAAGAAACAGAGCGCTTGAACATGTTGCAACTGGCAG 220
DB 121 GGAAGGCGCTTCCGCTCGCGAAGAAACAGAGCGCTTGAACATGTTGCAACTGGCAG 180
QY 221 TTGAGCGAGAAACCGGCGAGCATTTGCAATTTGCTGAGCTGCTATCCCGAGA 280
DB 181 TTGAGCGAGAAACCGGCGAGCATTTGCAATTTGCTGAGCTGCTATCCCGAGA 240
QY 281 GAGCCTGAGTGAATTTTGAATGATTTGCTGATTTGCTGATTTGCTGATTTGCTG 340
DB 241 GAGCCTGAGTGAATTTTGAATGATTTGCTGATTTGCTGATTTGCTGATTTGCTG 300
QY 341 GGTATATTTGAGGAATCACTTGGCAGAAATTTGGTTAAATGCTGAGAACTGCTGTC 400
DB 301 GGTATATTTGAGGAATCACTTGGCAGAAATTTGGTTAAATGCTGAGAACTGCTGTC 360
QY 401 CAAATCAAGCAAACTAATCTGTTGCTCAAGAGCTCTTGGCTGAGAACTGAGCA 460
DB 361 CAAATCAAGCAAACTAATCTGTTGCTCAAGAGCTCTTGGCTGAGAACTGAGCA 420
QY 461 GAGAATTCCTCAAGATGCTCGCGCTTCTCTCAACGAGAGCGCTTGGCAGGTTG 520
DB 421 GAGAATTCCTCAAGATGCTCGCGCTTCTCTCAACGAGAGCGCTTGGCAGGTTG 480
QY 521 TGTATGACGCTGAACCTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 580
DB 481 TGTATGACGCTGAACCTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 540
QY 581 TGATTTGAGCTGCTGACTACTTTTGAAGCTTACACTTTGTTTGAAGGAGAACTGCTC 640
DB 541 TGATTTGAGCTGCTGACTACTTTTGAAGCTTACACTTTGTTTGAAGGAGAACTGCTC 600
QY 601 ATGAGCTAGCTTCAAGGNACTTTTCTTATAGAGTGCCTTCCCTGCTGTTCCAGG 660
DB 661 ATGAGCTAGCTTCAAGGNACTTTTCTTATAGAGTGCCTTCCCTGCTGTTCCAGG 620
QY 699 AGACTGCTGATCCAGCTGAGATTTGCACTTGTATAGAAAAAATTACTGATGTT 758
DB 699 AGACTGCTGATCCAGCTGAGATTTGCACTTGTATAGAAAAAATTACTGATGTT 714
QY 759 GGAAC 763
DB 715 GGACC 719

RESULT 7
BE613468

| | | | | | |
|---------------------------|---|------------|------|--------|-----------------|
| LOCUS | BE613468 | 656 bp | mRNA | linear | EST-20-OCT-2000 |
| DEFINITION | 601504234p1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905984 5', mRNA sequence. | | | | |
| ACCESSION | BE613468 | | | | |
| VERSION | BE613468.1 | GI:9895065 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | human. | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| AUTHORS | 1 (bases 1 to 656) | | | | |
| TITLE | NIH-MGC http://mgc.nci.nih.gov/ . | | | | |
| JOURNAL | National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) | | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHM9714 row: c column: 09 High quality sequence stop: 643. Location/Qualifiers | | | | |
| FEATURES | 1..656 | | | | |
| source | /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3905984" /clone_lib="NIH_MGC_71" /tissue_type="telomysarcoma" /lab_host="DH10B (phage-resistant)" /note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb. | | | | |
| BASE COUNT | 160 a 153 c 184 g 159 t | | | | |
| ORIGIN | | | | | |
| Query Match | 23.8%; Score 622.2; DB 10; Length 656; | | | | |
| Best Local Similarity | 98.6%; Pred. NO. 2.4e-99; | | | | |
| Matches 638; Conservative | 0; Mismatches 8; Indels 1; Gaps 1 | | | | |
| QY | 22 GAGGGGTAGCAGGGTGGCGCTGGTGGGTGTGCAGGTCACCGAATCCCCAGAGA 81 | | | | |
| DB | 1 GAGGGGTGAGCAGGGTGGCGCTGGTGGGTGTGCAGGTCACCGAATCCCCAGAGA 60 | | | | |
| QY | 82 GGGGACTCTTAGAAGCCACCTGCTGTATTACCGGAGGAGGCGCCAGCCCGCC 141 | | | | |
| DB | 61 GGGGACTCTTAGAAGCCACCTGCTGTATTACCGGAGGAGGCGCCAGCCCGCC 120 | | | | |
| QY | 142 GAAGTCCTGGCAGCGCTCAGAAAGGCGCTGCGCTCGGAAAGAAACAGACCGTTGA 201 | | | | |
| DB | 121 GAAGTCCTGGCAGCGCTCAGAAAGGCGCTGCGCTCGGAAAGAAACAGACCGTTGA 180 | | | | |
| QY | 202 CCATGGTTGCACTGGCAATTTTGAGCAGCAAGACCGGCGCAGCATTTGCAATGCTGG 261 | | | | |
| DB | 181 CCATGGTTGCACTGGCAATTTTGAGCAGCAAGACCGGCGCAGCATTTGCAATGCTGG 240 | | | | |
| QY | 262 ACTGTGGCTATCACCCAGAGAGCGTGCCTAAGTAGATTTTACTACTGCGATTATGTTTTC 321 | | | | |
| DB | 241 ACTGTGGCTATCACCCAGAGAGCGTGCCTAAGTAGATTTTACTACTGCGATTATGTTTTC 300 | | | | |
| QY | 322 CTGAACCCCACTCAACAGCGATTATTTGAGGAATCAACTTGGCCAGAAATTTGGTTAAAA 381 | | | | |
| DB | 301 CTGAACCCCACTCAACAGCGATTATTTGAGGAATCAACTTGGCCAGAAATTTGGTTAAAA 360 | | | | |
| QY | 382 TGCCTGAGAACTGTCTGTCAATCAAAACAACTTAACTTGGTGGCTCAAGAGTCTCTTG 441 | | | | |
| DB | 361 TGCCTGAGAACTGTCTGTCAATCAAAACAACTTAACTTGGTGGCTCAAGAGTCTCTTG 420 | | | | |
| QY | 442 TCCCTGAGAACTGACGAGAGAAATTTGCTCAAGATGTCCTGCGGCTTTCTCAACGAGC 501 | | | | |

| QY | 421 | TCCTGTCAGAAACTGACCCAGAGAAATTGCTCAAGATGTCTCTGGGGCTTTTCTCTCAACGGAC | 480 |
|---------------------------|---|--|------|
| QY | 502 | CCTGGCGCTTGGCGAGGTGTGTATATGACGCTGAACCTTGGAAATTTGAAATGTATGTAAAA | 561 |
| DB | 481 | CTCGCGGCTTGGCGAGGTGTGTATATGACGCTGAACCTTGGAAATTTGAAATGTATGTAAAA | 540 |
| QY | 562 | ACCTGATGTAGATTTGGTGTGATTTAGCGGTGCTACTCTTTGAGCTTTACACTTGTCT | 621 |
| DB | 541 | ACCTGATGTAGATTCGTTGTGATTTAGCGGTGCTACTTAC-TTAGGAGCTTTACACTTGTCT | 599 |
| QY | 622 | TTAAGCAGAGAACTGCTCATGACTAGCTTAGGACTTTTCTT | 668 |
| DB | 600 | TTAAGCAGAGAACTGCTCATGACTAGCTTAGGACTTTTCTT | 646 |
| RESULT 8 | | | |
| LOCUS | BG428930 | 700 bp | mRNA |
| DEFINITION | 602500527P1 NIH_MGC_75 Homo sapiens CDNA clone IMAGE:4614127 5', | | |
| ACCESSION | BG428930 | | |
| VERSION | BG428930.1 | GI:13353436 | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| TITLE | 1 (bases 1 to 700) | | |
| JOURNAL | NIH-MGC http://mgc.ncl.nih.gov/. | | |
| COMMENT | National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) | | |
| | Contact: Robert Strausberg, Ph.D. | | |
| | Email: c9apbs-r@mail.nih.gov | | |
| | Tissue Procurement: Clontech Laboratories, Inc. | | |
| | CDNA Library Preparation: Clontech Laboratories, Inc. | | |
| | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) | | |
| | DNA Sequencing by: Incyte Genomics, Inc. | | |
| | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: | | |
| | http://image.llnl.gov | | |
| | Plate: L16M1365 row: e column: 08 | | |
| | High quality sequence stop: 690. | | |
| FEATURES | | | |
| source | Location/Qualifiers | | |
| | 1..700 | | |
| | /organism="Homo sapiens" | | |
| | /db_xref="taxon:9606" | | |
| | /clone="IMAGE:4614127" | | |
| | /clone_1lb="NIH-MGC_75" | | |
| | /lab_host="pH10B (T1 phage-resistant)" | | |
| | /note="Organ: kidney; vector: pDNR-LIB (Clontech); Site_1: SfilI (ggcgccctcgcc); Site_2: SfilI (ggccattatgcc); 5' adaptor 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTAATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCATGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC library." | | |
| BASE COUNT | 204 a 130 c 136 g 230 t | | |
| ORIGIN | | | |
| Query Match | 23 8%: Score 621.8: DB 10: Length 700: | | |
| Best Local Similarity | 97.4%: Pred. No. 2.8e-99: | | |
| Matches 685: Conservative | 0: Mismatches 12: Indels 6: Gaps 5 | | |
| QY | 1210 | GATATTAGCTATCAAACTTCGAAACCCACACACACACACTTCTCTGACTCAAAATTGA | 1269 |
| DB | 1 | GATATTAGCTATCAAACTTCGAAACCCACACACACACACTTCTCTGACTCAAAATTGA | 60 |
| QY | 1270 | AGGGTTTTAGACAGAGAGGTAGATTAAGTAGGTGATTAATTAAGCTTAACCTTAG | 1329 |
| DB | 61 | AGGGTTTTAGACAGAGAGGTAGATTAAGTAGGTGATTAATTAAGCTTAACCTTAG | 120 |

QY 1330 GTAGAGTAATGAGAAATATTACGGCAATATGAGAACTGCTTCTTCTTGCTGAC 1389
|||||
Db 121 GTAGAGTAATGAGAAATATTACGGCAATATGAGAACTGCTTCTTCTTGCTGAC 180
QY 1390 TTCCATCTAATAGTTTAAAGAGGCAAAAGCTATGCGCATTTGAGTACACAC 1449
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Db 181 TTCTCTACCTAATAGTTTAAAGAGGCAAAAGCTATGCGCATTTGAGTACACAC 240
QY 1450 GGTGTGTGTGTAGATGCTTTATAGCTCAGTTCCTTGTCTTCTTCTTCTTCTG 1509
|||||
Db 241 GGTGTGTGTGTAGATGCTTTATAGCTCAGTTCCTTGTCTTCTTCTTCTTCTG 300
QY 1510 TCTTTAACTAGAAATATGCAAAATATGAACTATTTCTGTGTAGTTTATTACTC 1569
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Db 301 TCTTTAACTAGAAATATGCAAAATATGAACTATTTCTGTGTAGTTTATTACTC 359
QY 1570 TTCCATCTAATAGTTTAAAGAGGCAAAAGCTATGCGCATTTGAGTACACAC 1629
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Db 360 TTCCATCTAATAGTTTAAAGAGGCAAAAGCTATGCGCATTTGAGTACACAC 419
QY 1630 CTCTCTGATTCAGTTAGTATCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1689
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Db 420 CTCTCTGATTCAGTTAGTATCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 479
QY 1690 GAACCATTTTACCATGAGTATCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1749
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Db 480 GAACCATTTTACCATGAGTATCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 539
QY 1750 TCTCTTAAACCCCAATGCTCAAGGTAGTACCTGATCTACATGCTTCTTCTTCT 1807
|||||
Db 540 TCTCTTAAACCCCAATGCTCAAGGTAGTACCTGATCTACATGCTTCTTCTTCT 599
QY 1808 AACGGTCAATTTAAGAACTCTGCAATGCTTCTTCTTCTTCTTCTTCTTCTTCT 1867
|||||
Db 600 AACGGTCAATTTAAGAACTCTGCAATGCTTCTTCTTCTTCTTCTTCTTCTTCT 657
QY 1868 AGATGAAGTCAAGCTGCTCAGA-TAACCATGATGACACCCAGA 1909
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Db 658 AGATGAAGTCAAGCTGCTCAGA-TAACCATGATGACACCCAGA 700

RESULT 9
BF969068 926 bp mRNA linear EST 22-JAN-2001
LOCUS 602270005F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4358112 5',
DEFINITION mRNA sequence.
ACCESSION BF969068.1 GI:12336283
VERSION BF969068
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Homindae; Homo.
TITLE NIH-bases 1 to 926)
JOURNAL http://imgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM995 row: j column: 01
High quality sequence stop: 672.
Location/Qualifiers
1..926

FEATURES
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/db_xref="taxon:9606"

/clone="IMAGE:4358112"
/clone_lib="NIH_MGC_84"
/lisse_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-Sport6; Site: 1:
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 232 a 201 c 200 g 293 t
ORIGIN

Query Match 23.4%; Score 612; DB 10; Length 926;
Best Local Similarity 96.2%; Pred. No. 1.3e-97;
Matches 691; Conservative 0; Mismatches 20; Indels 7; Gaps 6;

QY 1543 GATATTTCTGTGTAGTATTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1602
|||||
Db 29 GATATTTCTGTGTAGTATTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 88
QY 1603 TAGGAATGAGTTCTGAGATCTAGTCCCTCTGATCTTCTTCTTCTTCTTCTTCT 1662
|||||
Db 89 TAGGAATGAGTTCTGAGATCTAGTCCCTCTGATCTTCTTCTTCTTCTTCTTCT 148
QY 1663 CAGTATTTACATGCTTATATCTGATGACATTTTACATGACGATGATCTATCT 1722
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Db 149 CAGTATTTACATGCTTATATCTGATGACATTTTACATGACGATGATCTATCT 208
QY 1723 CTGGGCTTTTCTGGGAATGAGTATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1782
|||||
Db 209 CTGGGCTTTTCTGGGAATGAGTATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 268
QY 1783 GTATATCTACCTTTGAATTTATGAAAGGGTCAATTTATGCAAGTCTGCTATG 1842
|||||
Db 269 GTATATCTACCTTTGAATTTATGAAAGGGTCAATTTATGCAAGTCTGCTATG 328
QY 1843 AGATATGTTTATGATGACCTTAGAATGAAAGTCAAGCTGCTGATGATGATG 1902
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Db 329 AGATATGTTTATGATGACCTTAGAATGAAAGTCAAGCTGCTGATGATGATG 388
QY 1903 ACCCAGATTTTCTCCACCTTGGATACCTGCTCACTAGAGGAATTAAGGCTGATTTT 1962
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Db 389 ACCCAGATTTTCTCCACCTTGGATACCTGCTCACTAGAGGAATTAAGGCTGATTTT 448
QY 1963 GCTTATTTCCAACTAATGATCATTTATCTCTTCTTCTTCTTCTTCTTCTTCT 2022
|||||
Db 449 GCTTATTTCCAACTAATGATCATTTATCTCTTCTTCTTCTTCTTCTTCTTCT 508
QY 2023 AGCCTCCACTCAACAATGTTCAATTCAGCAAGGCTTCTTCTTCTTCTTCTTCT 2082
|||||
Db 509 AGCCTCCACTCAACAATGTTCAATTCAGCAAGGCTTCTTCTTCTTCTTCTTCT 568
QY 2083 ATAGAGAGCTTATTCAGG-TTTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCT 2139
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Db 569 ATAGAGAGCTTATTCAGGTTTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCT 628
QY 2140 GACTGCGGTAGGAGACATGATCTCTGCTGTTTCTTCTTCTTCTTCTTCTTCT 2199
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Db 629 GACTGCGGTAGGAGAC-GATGATTCATCTGCTGTTTCTTCTTCTTCTTCTTCT 686
QY 2200 TGTGATCTATTAAGTCACTTAATGTCATGTTCAATTTAGCAAGTCTTCTTCT 2257
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Db 687 TGTGATCTATTAAGTCACTTAATGTCATGTTCAATTTAGCAAGTCTTCTTCT 742

RESULT 10
BM470629 1211 bp mRNA linear EST 05-FEB-2002
LOCUS BM470629
DEFINITION AGENCOURT 6463144 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5533483
ACCESSION BM470629
VERSION BM470629.1 GI:18519671
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE NIH-MGC (bases 1 to 1211)
JOURNAL Unpublished (1999)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLML218 row: 9 column: 20
High quality sequence start: 4
High quality sequence stop: 607.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:553483"
/clone_lib="NIH-MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 269 a 353 c 305 g 281 t 1 others
ORIGIN
Query Match 23.3%; Score 609.2; DB 10; Length 1211;
Best Local Similarity 98.6%; Pred. No. 3.7e-97;
Matches 625; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 542 AATTGAAATGATATGTAAGCTGATGATTTGTGTGATTTACGCTGACCTA- 600
|||||
DB 570 AATTGAAATGATATGTAAGCTGATGATTTGTGTGATTTACGCTGACCTA- 629
QY 601 CTTTGTAGCTTACCTGTTGTTTACGAGAGAA 634
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DB 630 CTTTGTAGCTTACCTGTTGTTTACGAGAGAA 663
RESULT 11
BM472975 1435 bp mRNA .linear EST 05-FEB-2002
LOCUS AGENCOURT_6462582 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5519576
DEFINITION 5', mRNA sequence.
ACCESSION BM472975
VERSION BM472975.1 GI:18522017
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE NIH-MGC (bases 1 to 1435)
JOURNAL Unpublished (1999)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLML2182 row: 8 column: 09
High quality sequence start: 53
High quality sequence stop: 454.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 416 a 338 c 264 g 416 t 1 others
ORIGIN
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Best Local Similarity 93.7%; Pred. No. 3.5e-97;
Matches 635; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

http://image.lnl.gov
Plate: LLM9735 row: 1 column: 11
High quality sequence stop: 647.
Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 211 a 199 c 243 g 210 t
ORIGIN

Query Match 23.1%; Score 602.4; DB 10; Length 863;

Best Local Similarity 90.0%; Pred. No. 6.4e-96;
Matches 718; Conservative 0; Mismatches 61; Indels 19; Gaps 6;

Db 23 AGGGGTGACAGAGGTCGGCTGCTGGGGTCTGCAGGTACCGAGTCCCGAGAGAG 82
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1 AGGGGTGACAGAGGTCGGCTGCTGGGGTCTGCAGGTACCGAGTCCCGAGAGAG 60
83 GGGACTCTTAAGAACCACTGCTGTGTTAACCGGACGAGCGCCAGCCCGCG 142
61 GGGACTCTTAAGAACCACTGCTGTGTTAACCGGACGAGCGCGAGCGCCCGCG 120
143 AACCTCTGACAGCGCTGACAGAAAGCGCTGGCGCTCGCGAAGAAACAGAGCCCTTAC 202
121 AACCTCTGACAGCGCTGACAGAAAGCGCTGGCGCTCGCGAAGAAACAGAGCCCTTAC 180
203 CATGTTCACTGACATTTGAGCAGCAGAACCCGGCCAGCATTTGAGATTGCTGGA 262
181 CATGTTCACTGACATTTGAGCAGCAGAACCCGGCCAGCATTTGAGATTGCTGGA 240
263 CTGTGCTATACCCAGAGAGCTGCTAAGTATTTGACTACTGCGATTTATGTTCTCC 322
241 CTGTGCTATACCCAGAGAGCTGCTAAGTATTTGACTACTGCGATTTATGTTCTCC 300
323 TGAACCCCAACCTCAAGAGGTAAATTTGAGGAATCAACTGGCAATTTGGTAAAT 382
301 TGAACCCCAACCTCAAGAGGTAAATTTGAGGAATCAACTGGCAATTTGGTAAAT 360
383 GCTGAGAGACTGTCTGTCCAAATCAAGCAAACTAAGTGGTCTCAAGAGTCTTGT 442
361 GCTGAGAGACTGTCTGTCCAAATCAAGCAAACTAAGTGGTCTCAAGAGTCTTGT 420
443 CCCTGAGAACTGACGACAGAGATTGTCAGAGTCTCTGGCGCTTCTCTCAAGCGAGCC 502
421 CCCTGAGAACTGACGACAGAGATTGTCAGAGTCTCTGGCGCTTCTCTCAAGCGAGCC 480
503 CTGGCGCTTGGAGGTTGTTATATGACAGTGAACCTTGAATTTGAATTTGTAATAA 562
481 CTGGCGCTTGGAGGTTGTTATATGACAGTGAACCTTGAATTTGAATTTGTAATAA 539
563 GCTGATAGGATTGTGTGATTTAGAGGTGCTACTTCTTTGAGCTTACACTGTGT 622
540 GCTGATAGGATTGTGTGATTTAGAGGTGCTACTTCTTTGAGCTTACACTGTGT 599
623 TTAAGCAGGA--GAAGTCTCAT--GGACTAGCTT--CAGGAGCTTTTCTT---TAGTAG 673
600 TTAAGCAGGAAGAACTGCTCATGAGCTAGCTTTTCAAGGAGCTTTTCTTTTGAATGAG 659
674 AGGTGCTTCTCTCTCTGTTTCAAGAGAACTGATCTCTGAGTCAAGATTTCCAGT-- 731
660 AGTGGCTTCTCTCTCTGTTTCCAGAGAAAGCTGTGAGTCAAGATTTCCAGATTTTC 719
732 -----GTTAAGAAAACTTTACTCACTGATTGGAACAACAGTATGGAAGGCTCTTA 784
720 GGACTCGGTATGAAGAAACCTTTCTCCCTGGTGGGACACAGGCGTTTGAAGGCGCC 779

Qy 785 AAAAGGAAAAATATATAA 802
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Db 780 CCAAGGAAACACTTAA 797

RESULT 14

BF791321 832 bp mRNA linear EST 12-JAN-2001
LOCUS 602250867.1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338064 5',
DEFINITION mRNA sequence.
BF791321
ACCESSION BF791321.1 GI:12096375
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 832)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM1213 row: f column: 17
High quality sequence stop: 589.
Location/Qualifiers

FEATURES

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/clone_id="NIH_MGC_81"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggcgccctcgccg); Site_2: SfiI
(ggcgattatggc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGGCACATG-dT(30)-BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
BASE COUNT 252 a 148 c 175 g 257 t
ORIGIN

Query Match 22.3%; Score 583.2; DB 10; Length 832;
Best Local Similarity 95.7%; Pred. No. 1.5e-92;
Matches 674; Conservative 0; Mismatches 23; Indels 7; Gaps 7;

Qy 717 TCAGATTTTCGACTGTTAAGAAAAAAGCTTCTACTGATTTGAACAGTGA 776
Db 1 TCAGATTTTCGACTGTTAAGAAAAAAGCTTCTACTGATTTGAACAGTGA 60
777 GGGTCTTAAAAAGGAAAAATATATTAAGATTATTTTATGATTTGGTAGTAAACTATTTCA 836
Db 61 GGGTCTTAAAAAGGAAAAATATATTAAGATTATTTTATGATTTGGTAGTAAACTATTTCA 120
Qy 837 GCTATCAGCTAAATGCTATTGTACTTTGGCCCACTGCGCTTAATTAAGAAACCCCAAT 896
Db 121 GCTATCAGCTAAATGCTATTGTACTTTGGCCCACTGCGCTTAATTAAGAAACCCCAAT 180
897 GTAGTCTCTTTCTTCTGTGTGTTCACATTCATTAACAAGTCAAGAGTCAAGGCTGATTTT 956
Db 181 GTAGTCTCTTTCTTCTGTGTGTTCACATTCATTAACAAGTCAAGAGTCAAGGCTGATTTT 240

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QY 957 CTGGCTTTGGAGAAGTATTCATATAGTATTTTCGATAGATCCATTTTTGT 1016
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Db 241 CTGGCC-CTTGAGAGAGTATTCATATAGTATTTTCGATAGATCCCA-TTTTGT 298
QY 1017 ACAGAAATGATGGGATAGTATAGTAAAGCAAAAGTACAGCCATTGAGTTTACAT 1076
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 ACAGAAATGATGGGATAGTATAGTAAAGCAAAAGTACAGCCATTGAGTTTACAT 358
QY 1077 TGATTCACAAATTTGTTTCAGTAGAGCTTGATAGATATATAACAGATTGGCT 1136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 TGATTCACAA-CTTGTTTCAGTAGAGCTTGATAGATATATAACAGATTGGCT 417
QY 1137 ATTTGATTTTCATATAGCTTTTTCCTGTAAGTTTTCAGAGATTTTAAATCACAG 1196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 A-TTTGATTTTCATATAGCTTTTTCCTGTAAGTTTTCAGAGATTTTAAATCACAG 476
QY 1197 AATCATCTAATATATATTTTTCATCAAAAGCTTCCAAAAGCCACACAGCTTCT 1256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 AATCATCTAATATATATTTTTCATCAAAAGCTTCCAAAAGCCACACAGCTTCT 536
QY 1257 GACTCAAAATTTGAAGGCTTTT-AGACAGAGGAGTATAGTATAGTATAGTATAT 1314
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Db 537 GACTCAAAATTTGAAGGCTTTTTCAGACAGGAGTATAGTATAGTATAGTATAT 596
QY 1315 AAGCTTAACCTAGTATAGTATAGTATATAGTATAGTATAGTATAGTATAGTAT 1374
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Db 597 AAGCTTAACCTAGTATAGTATAGTATATAGTATAGTATAGTATAGTATAGTAT 655
QY 1375 CTGTTCTTGGTGAATCCCTCCTATATATTTTAAAGAGCA 1418
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RESULT 15
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LOCUS 601660234R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905984 3',
DEFINITION mRNA sequence.
ACCESSION BE966555
VERSION BE966555.2 GI:11772097
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 941)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            On Oct 3, 2000 this sequence version replaced gi:10577280.
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LMU at:
            http://image.llnl.gov
            Plate: LNCM701 row: c column: 09
            High quality sequence stop: 642.
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FEATURES
SOURCE
BASE COUNT 336 a 172 c 209 g 224 t

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ORIGIN
Query Match 22.3%; Score 582.4; DB 10; Length 941;
Best Local Similarity 94.6%; Pred. No. 2e-92;
Matches 668; Conservative 0; Mismatches 31; Indels 7; Gaps 6;

QY 1901 GCACCCAGATTTTTCACCTTGATACCTGTCACTAGGAGATTAAGGCTTGATTT 1960
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Db 700 GCACCCAGAGTGTCTTCCAC--CGGATACCGTCACTAGGAGATTAAGGCTTGATTT 644
QY 1961 TTGCTTTTCCACTAGTATAGTATATCTCTTCTTTTATATGTAAGAGAGAT 2020
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 TTGCTTTTCC-ACCTAGTATAGTATATCTCTTCC--TTTATGTAAGAGAGAT 586
QY 2021 TTAGCTTCACACACACA-ATGTTCAATTCAGCAAGGCTTTCATCTCTGCTGGTGC 2079
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 585 TTAGCTTCACACACACATATGTTCAATTCAGCAAGGCTTTCATCTCTGCTGGTGC 526
QY 2080 TGGATTAAGAGCTTATTTCAAGTTTCTGCTAGCTATTTAGCTCCACTTCACATCTGGA 2139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 525 TGGATTAAGAGCTTATTTCAAGTTTCTGCTAGCTATTTAGCTCCACTTCACATCTGGA 466
QY 2140 GACTGCGTAGGAGACAGATGTATTCATCTGCTGTTAGTGAAGAGAGGTGATCTGT 2199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 465 GACCGGCGTAGGAGACAGATGTATTCATCTGCTGTTAGTGAAGAGAGGTGATCTGT 406
QY 2200 TAGTGTACTATTAAGTGAACCTAAATGTCATCTGTTCAAAATTAAGCAAGTCTTAACAAC 2259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 405 TACTGATACTATTAAGTGAACCTAAATGTCATCTGTTCAAAATTAAGCAAGTCTTAACAAC 346
QY 2260 TAAACTCTTCAAAATCTGTTGAAGATTAACAAACCAATCTTATAGATTTGGCCCAAG 2319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 345 TAAACTCTTCAAAATCTGTTGAAGATTAACCAACCAATCTTATAGATTTGGCCCAAG 286
QY 2320 ATAAATCTATGTGTTTGCATAGCTATTTAGCTCCAAAGTTCATCTGTTTCTGC 2379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 ATAAATCTATGTGTTTGCATAGCTATTTAGCTCCAAAGTTCATCTGTTTCTGC 226
QY 2380 CGCTGTCTGAGATGTCACACAGTGAAGGCTTCTGTCATAGATAGTGAAC 2439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 CGCTGTCTGAGATGTCACACAGTGAAGGCTTCTGTCATAGATAGTGAAC 166
QY 2440 GTTGTCTTCTTCCCACTAAAGTATATCTGCTCTGCTGTTATGCTTACAAATG 2499
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Db 165 GTTGTCTTCTTCCCACTAAAGTATATCTGCTCTGCTGTTATGCTTACCAATG 106
QY 2500 GTGATGCTTATGAAGGCTGTTAAATTAATATCTGCTGTTAAAGGAAATTAAGTTTGTG 2559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 105 GTGATGCTTATGAAGGCTGTTAAATTAATATCTGCTGTTAAAGGAAATTAAGTTTGTG 46
QY 2560 TATTTTGAACATTAACATTAATATATTTTAAAGGAAATTAAGTTTGTG 2605
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Db 45 TATTTTGAACAT- AAACCTTATATATTTTAAAGGAAATTAAGTTTGTG 1

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Search completed: October 13, 2002, 03:52:21
 Job time : 2985 secs

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar

[illegible]

| | | | |
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| 0Y | 766 | CAGTATATGAAAGGCGCTAAAAAGGAAAAATATTAAGACATATTTCAATGATGGCTAGT | 825 |
| Db | 24112 | CAGTATATGAAAGGCGCTAAAAAGGAAAAATATTAAGATATTTCAATGATGGCTAGT | 24171 |
| 0Y | 826 | AAATCATTCACGCTAGTACGCTAAAGTCATTTGTAGTTGGCCCACTGCCCTAATATAG | 885 |
| Db | 24112 | AAATCATTCACGCTAGTACGCTAAAGTCATTTGTAGTTGGCCCACTGCCCTAATATAG | 24231 |
| 0Y | 886 | AAACCCCAATGTAGTCTCTTTTCTTTCTGTGTTTCACATTCATAGCACTGCAGCTAAC | 945 |
| Db | 24232 | AAACCCCAATGTAGTCTCTTTTCTTTCTGTGTTTCACATTCATAGCACTGCAGCTAAC | 24291 |
| 0Y | 946 | AGGCGATTTTCCTGGCCCTTGGAGAAAGTATCAAAATATAGTACATTTTCGCAATAGT | 1005 |
| Db | 24292 | AGGCGATTTTCCTGGCCCTTGGAGAAAGTATCAAAATATAGTACATTTTCGCAATAGT | 24351 |
| 0Y | 1006 | CCCATTTTGTATCAGAAATTTGAATGGATGGATAGTAAAGTAAAGTAAAGCCATTGTG | 1065 |
| Db | 24352 | CCCATTTTGTATCAGAAATTTGAATGGATGGATAGTAAAGTAAAGTAAAGCCATTGTG | 24411 |
| 0Y | 1066 | AGTTTTCATTTTGATTCACAATTTGGTTTCAGTAGGCGTTGGTATAGACTATATTAAC | 1125 |
| Db | 24412 | AGTTTTCATTTTGATTCACAATTTGGTTTCAGTAGGCGTTGGTATAGACTATATTAAC | 24471 |
| 0Y | 1126 | CAGATTTGGCTATTTTGTGATTTTCATATGGCTTTTTTTTCTGTAACTTTTCAGAGATTTT | 1185 |
| Db | 24472 | CAGATTTGGCTATTTTGTGATTTTTCATATGGCTTTTTTTTCTGTAACTTTTCAGAGATTTT | 24531 |
| 0Y | 1186 | TTTAATATCAGAGATATATCTAATATATATTTAGCTATCAAACTTCCAAAAGCCACAC | 1245 |
| Db | 24532 | TTTAATATCAGAGATATATCTAATATATATTTAGCTATCAAACTTCCAAAAGCCACAC | 24591 |
| 0Y | 1246 | CACGAGTTCCCTGACTCAAAATTTTGAAGGGTTTTTATAGACAGAGGGTAGATTAAATAGTG | 1305 |
| Db | 24592 | CACGAGTTCCCTGACTCAAAATTTTGAAGGGTTTTTATAGACAGAGGGTAGATTAAATAGTG | 24651 |
| 0Y | 1306 | AATTTAATTAAGGCTAATACCCCTAGGTAAAGATAGATTAATATTTACGGCAATATATGA | 1365 |
| Db | 24652 | AATTTAATTAAGGCTAATACCCCTAGGTAAAGATAGATTAATATTTACGGCAATATATGA | 24711 |
| 0Y | 1366 | ACTGCTTCACTGTTTCTTGTTGATCTTCCATCAGTCAATGTTTAAAGAGGCAACAAAAGC | 1425 |
| Db | 24712 | ACTGCTTCACTGTTTCTTGTTGATCTTCCATCAGTCAATGTTTAAAGAGGCAACAAAAGC | 24771 |
| 0Y | 1426 | TTATGCTGCCATTTGATTAACCAACGGGTGTTGTTTAGATGCTTTATTAAGCTCAGGTTCC | 1485 |
| Db | 24772 | TTATGCTGCCATTTGATTAACCAACGGGTGTTGTTTAGATGCTTTATTAAGCTCAGGTTCC | 24831 |
| 0Y | 1486 | CTTGTTCTTAAGGTGTAATTAAGTCTTTAACTGAAAAAGCAAAATATTTGAAGTATGAT | 1545 |
| Db | 24832 | CTTGTTCTTAAGGTGTAATTAAGTCTTTAACTGAAAAAGCAAAATATTTGAAGTATGAT | 24891 |
| 0Y | 1546 | ATTTCCTGTGTAGTTTATTTACTCTTCCATGTAGTGAATGATTAACCTGTGAGGATATAG | 1605 |
| Db | 24892 | ATTTCCTGTGTAGTTTATTTACTCTTCCATGTAGTGAATGATTAACCTGTGAGGATATAG | 24951 |
| 0Y | 1606 | GAATATGAGTTCTGAGATCTAGTCCCTCTCTGTGATTCACCTAGTATATCTATCTTTTCAG | 1665 |
| Db | 24952 | GAATATGAGTTCTGAGATCTAGTCCCTCTCTGTGATTCACCTAGTATATCTATCTTTTCAG | 25011 |
| 0Y | 1666 | TATTCATGATGCTTATATCTCAGATGACCATTTTCACATGCGCATGTTATCTCATCTCTG | 1725 |
| Db | 25012 | TATTCATGATGCTTATATCTCAGATGACCATTTTCACATGCGCATGTTATCTCATCTCTG | 25071 |
| 0Y | 1726 | GGCTTTTCGGGAATTTGAAGTATATCTCTCTTAACCCCAATTTTCAAGGGTAACTAGCTGTA | 1785 |
| Db | 25072 | GGCTTTTCGGGAATTTGAAGTATATCTCTCTTAACCCCAATTTTCAAGGGTAACTAGCTGTA | 25131 |
| 0Y | 1786 | TACTACCACTTTGAATATTTAAAGAGGCGCATATTTACGAAGCTCATTTGCGCTATGGAGA | 1845 |
| Db | 25132 | TACTACCACTTTGAATATTTAAAGAGGCGCATATTTACGAAGCTCATTTGCGCTATGGAGA | 25191 |
| 0Y | 1846 | TATGTTTATATAGTACAGCCTAGAGATGAAGTATCAACGCTCAGATTAACCATGATCATCAC | 1905 |

[illegible]

JOURNAL Submitted (11-DEC-2000) CNRS, Faculte des Sciences, UMR 6548, Parc
Valrose, Nice 06108, France
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/clone="03A12"
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1..1107
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439..1020
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LRGCVHVNLEIENVCCKIDRIYCDASVPEPLTLVFKOESCWTSLSKDFPSGRF
SSGLRTRLSSFRVKKKLYSLIGTVIEEC"

BASE COUNT 344 a 207 c 260 g 296 t
ORIGIN

Query Match 20.1% Score 523.6; DB 10; Length 1107;
Best Local Similarity 84.9%; Pred. No. 4.2e-115;
Matches 566; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 161 GGAAGGCCGTTGCGCTCGCGAAGAACAGAGCCCTTGACATGCTGTCACACTGCAG 220
DB 396 GAAAGATCCGTTCTGCTCGCGAGGAAACAGAGCCGTTACATGTTGCAACGGGCGAG 455
QY 221 TTGGAGCAGCAAGAACCGCGCAGCATTTGAGAAATTCCTGAGCTGTGGCTATCCAGCA 280
DB 456 TTGGAGCAGCAAGAACCGCGCAGCATTTGAGAAATTCCTGAGCTGTGGCTATCCAGCA 515
QY 281 GAGCCTGCTAAGTATTTGACTACTGAGATTTGTTGTTGCTGCTGACCCCAACCTCAACGA 340
DB 516 GAGTCTGCTAAGTATTTGACTACTGAGATTTGTTGTTGCTGCTGACCCCAACCTCAACGA 575
QY 341 GGTAAATATTTGAGAAATCAACTGCGCAGAAATTTGGTTAAATGCTGAGAACTGCTGTC 400
DB 576 GGTGTTGTTGAGAAATCAACTGCGCAGAAATTTGGTTAAATGCTGAGAACTGCTGTC 635
QY 401 CAATCAAGCAAACTAACTGCTGCTCAAGAGTCTTGTCCCTGAGAACTGAGCA 460
DB 636 CAAGTCAAGCAAACTAACTGCTGCTCAAGAGTCTTGTCCCTGAGAACTGAGCA 695
QY 461 GAGAATGCTCAAGATGCTGCGGCTTCTCAAGAGAGCCGCGGCTTGCGAGGTG 520
DB 696 GAGAATGCTCAAGATGCTGCGGCTTCTCAAGAGAGCCGCGGCTTGCGAGGTG 755
QY 521 TGTATGACAGTGAATTTGAAATGTATGTAATAAAGCTGATAGATTTGTGTG 580
DB 756 TGTATGACAGTGAATTTGAAATGTATGTAATAAAGCTGATAGATTTGTGTG 815
QY 581 TGTATGACAGTGAATTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTG 640
DB 816 TGTATGACAGTGAATTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTG 875
QY 641 ATGAGACTAGCTTGAAGACTTTTCTTTAGTAGAGTGCCTTCTGCTGCTGCTGCTGCTGCTG 700
DB 876 CTGAGACAGCTTCAAGAGCTTTCTTTAGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935
QY 701 AACTGATGCTTCAAGCTTCAAGATTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTG 760
DB 936 AACTGATGCTTCAAGCTTCAAGATTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTGAGCTTTG 995
QY 761 AACCAAGCTTGAAGAGTCTTAAAGAAAGAAATATATAAGATATATTCATGATGTTG 820
DB 996 AACCAAGCTTGAAGAGTCTTAAAGAAAGAAATATATAAGATATATTCATGATGTTG 1055
QY 821 GTAGTAAACCTATTCAGCTAGTGAAGTAA 850

DB 1056 CTAATAAACCTCTGAGCTATCCAGCAAA 1085

RESULT 4
AF335325 667 bp mRNA linear ROD 06-DEC-2001
LOCUS AF335325
DEFINITION Mus musculus Rtp801-like protein mRNA, complete cds.
ACCESSION AF335325
VERSION AF335325.1 GI:17385766
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 667)
Shoshani,T., Faerman,A., Met,I., Zelin,E., Tenne,T., Gorodin,S.,
Moshe,Y., Elbaz,S., Budanov,A., Chajut,A., Kalinski,H., Kamer,I.,
Rosen,A., Mor,O., Keshet,E., Leshkowitz,D., Eilat,P., Skallier,R.
and Feinstein,E.,
Identification of a novel HIF-1 responsive gene Rtp801 involved in
apoptosis
Mol. Cell. Biol. (2002) In press

TITLE
JOURNAL 2 (bases 1 to 667)
REFERENCE Shoshani,T., Faerman,A., Met,I., Zelin,E., Tenne,T., Gorodin,S.,
AUTHORS Moshe,Y., Elbaz,S., Budanov,A., Chajut,A., Kalinski,H., Kamer,I.,
Rosen,A., Mor,O., Keshet,E., Leshkowitz,D., Eilat,P., Skallier,R.
and Feinstein,E.,
Direct Submission
Submitted (10-JAN-2001) Research Division, QBI Enterprises Ltd.,
P.O. Box 4071, Ness-Ziona 70400, Israel

TITLE
JOURNAL
P.O. Box 4071, Ness-Ziona 70400, Israel

FEATURES

source 1..667
/organism="Mus musculus"
/db_xref="taxon:10090"
64..645
/note="Rtp801L"
/codon_start=1
/product="Rtp801-like protein"
/protein_id="ALU38425.1"
/db_xref="GI:17385767"
/translation="MVATGSLSSKNPASISELLDGGSHPSLSDPDMYVYVPEPL
NEVFEETCONVKMLKENSCKOTKLGCSVLPKLTORIADIVLRISTEPCG
LRGCVHVNLEIENVCCKIDRIYCDASVPEPLTLVFKOESCWTSLSKDFPSGRF
SSGLRTRLSSFRVKKKLYSLIGTVIEEC"

BASE COUNT 170 a 149 c 184 g 164 t
ORIGIN

Query Match 20.0% Score 522.4; DB 10; Length 667;
Best Local Similarity 88.2%; Pred. No. 7.6e-115;
Matches 566; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 161 GGAAGGCCGTTGCGCTCGCGAAGAACAGAGCCCTTGACATGCTGTCACACTGCAG 220
DB 21 GAAAGATCCGTTCTGCTCGCGAGGAAACAGAGCCGTTACATGTTGCAACGGGCGAG 80
QY 221 TTGGAGCAGCAAGAACCGCGCAGCATTTGAGAAATTCCTGAGCTGTGGCTATCCAGCA 280
DB 81 TTGGAGCAGCAAGAACCGCGCAGCATTTGAGAAATTCCTGAGCTGTGGCTATCCAGCA 340
QY 281 GAGCCTGCTAAGTATTTGACTACTGAGATTTGTTGTTGCTGCTGACCCCAACCTCAACGA 340
DB 141 GAGTCTGCTAAGTATTTGACTACTGAGATTTGTTGTTGCTGCTGACCCCAACCTCAACGA 400
QY 341 GGTAAATATTTGAGAAATCAACTGCGCAGAAATTTGGTTAAATGCTGAGAACTGCTGTC 400
DB 201 GGTGTTGTTGAGAAATCAACTGCGCAGAAATTTGGTTAAATGCTGAGAACTGCTGTC 460
QY 401 CAATCAAGCAAACTAACTGCTGCTCAAGAGTCTTGTCCCTGAGAACTGAGCA 460
DB 261 CAGATCAAGCAAACTAACTGCTGCTCAAGAGTCTTGTCCCTGAGAACTGAGCA 320
QY 461 GAGAATGCTCAAGATGCTGCGGCTTCTCAAGAGAGCCGCGGCTTGCGAGGTG 520

|||||
Db 321 GAGAAATTCCTCAAGATGTCGCGGCTCTCGTCCACGAGCCCTCGGCGCTTCGCGGTTG 380
Qy 521 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 580
Db 381 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 440
Qy 581 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 640
Db 441 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 500
Qy 641 ATGACCTAGCTTCAAGGACCTTTTCTTTAGTAGAGTGGCTTCTGCTGTTTCAGAG 700
Db 501 GTGACACGCTTCAAGGACCTTTCTTTAGTAGAGTGGCTTCTGCTGTTTCAGAG 560
Qy 701 AACCTGATCTGACGCTGAGATTGCGACTGTGTAAAGAAAACCTTCTCAGATTGG 760
Db 561 AACCTGATCTGACGCTGAGATTGCGACTGTGTAAAGAAAACCTTCTCAGATTGG 620
Qy 761 AACACACTGATTGAAGGCTCTTAAAGGAAATATATTAAG 804
Db 621 AACGACACTCATTTGAAGAGTGTCTAAGAGAGAAACATTAAG 664
RESULT 5
AX268802 867 bp DNA linear PAT 29-OCT-2001
LOCUS AX268802
DEFINITION Sequence 3 from Patent WO0174901.
ACCESSION AX268802
VERSION AX268802.1 GI:16541861
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (sites)
AUTHORS Stanton, L.W. and White, R.T.
TITLE Secreted factors
JOURNAL Patent: WO 0174901-A 3 11-OCT-2001;
Scienc. Inc. (US)
FEATURES
source location/Qualifiers
1..867
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
BASE COUNT 204 a 202 c 245 g 199 t 17 others
ORIGIN
Query Match 19.6%; Score 511; DB 6; Length 867;
Best Local Similarity 85.0%; Pred. No. 4,3e-112;
Matches 571; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 161 GAAAGCCGCTGGCGCGGGAAGAAAGAGCGCTTGAACATGATGGCAG 220
Db 172 GAAAGATCCGTTCTGCTCGCGAGGAAACAGAGCGCTTGAACATGATGGCAG 231
Qy 221 TTGAGCAGCAGAACCCGCGGACGATTTGCAATTTGCTGCACTGTGCTATCACCCAGA 280
Db 232 TTGAGCAGCAGAACCCGCGGACGATTTGCAATTTGCTGCACTGTGCTATCACCCAGA 291
Qy 281 GAGCTGCTAGTATTTGACTACTGGGATTTATTTGTTCTGTAACCACTAAGCA 340
Db 292 GAGCTGCTAGTATTTGACTACTGGGATTTATTTGTTCTGTAACCACTAAGCA 351
Qy 341 GGTATATTTGAGGATCACTTGGCAGATTTGGTAAATGCTGGAGAACTGTCTGTC 400
Db 352 GGTGCTGTTGAAGAGACATGCGCAGATTTGGTAAATGCTGGAGAACTGTCTGTC 411
Qy 401 CAAATCAAGCAAACTAATTTGTTGCTCAAGGCTCTGCTGTAAGAACTGACCA 460
Db 412 CAAATCAAGCAAACTAATTTGTTGCTCAAGGCTCTGCTGTAAGAACTGACCA 471
Qy 461 GAGAAATTCCTCAAGATGTCGCGGCTCTCGTCCACGAGCCCTCGGCGCTTCGCGAGTTG 520

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Db 472 GAGAAATTCCTCAAGATGTCGCGGCTCTCGTCCACGAGCCCTCGGCGCTTCGCGGTTG 531
Qy 521 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 580
Db 532 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 591
Qy 581 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 640
Db 592 TGTATGACGCTGAACTGGAAATGTATGTAAAAAGCTGGATAGATTGTGTG 651
Qy 641 ATGACCTAGCTTCAAGGACCTTTTCTTTAGTAGAGTGGCTTCTGCTGTTTCAGAG 700
Db 652 GTGACACGCTTCAAGGACCTTTCTTTAGTAGAGTGGCTTCTGCTGTTTCAGAG 711
Qy 701 AACCTGATCTGACGCTGAGATTGCGACTGTGTAAAGAAAACCTTCTCAGATTGG 760
Db 712 AACCTGATCTGACGCTGAGATTGCGACTGTGTAAAGAAAACCTTCTCAGATTGG 771
Qy 761 AACACACTGATTGAAGGCTCTTAAAGGAAATATATTAAGATTTATTCATGATTGG 820
Db 772 AACGACACTCATTTGAAGAGTGTCTAAGAGAGAAACATTAAGTCTCATTAGATTGG 831
Qy 821 GTAGTAAACTA 832
Db 832 CTAAACAAAANA 843

RESULT 6
AF327512 639 bp mRNA linear ROD 09-DEC-2001
LOCUS AF327512
DEFINITION Mus musculus SMH51 (Smh51) mRNA, complete cds.
ACCESSION AF327512
VERSION AF327512.1 GI:17432246
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 639)
AUTHORS Cros, N., Tkatchenko, A.V., Leclerc, L., Leger, J.J., Marini, J.-F. and
Dechesne, C.A.
TITLE Gene expression alterations revealed by suppression subtractive
hybridization in rat soleus muscle disuse atrophy
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 639)
JOURNAL Direct Submission
TITL Leclerc, L., Pisanil, D.F., Cros, N. and Dechesne, C.A.
JOURNAL Submitted (11-DEC-2000) CNRS, Faculte des Sciences, UMR 6548, Parc
Valrose, Nice 06108, France
FEATURES
source location/Qualifiers
1..639
/organism="Mus musculus"
/strain="C57BL/10ScSn"
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/clone="03A12"
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1..639
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19..600
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NEVVEFTTQNLVKNLENCISRSKQTKLGCSKVLVPEKLTQRTAODVLRISTPEPG
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BASE COUNT 166 a 136 c 173 g 164 t
ORIGIN
Query Match 19.5%; Score 509; DB 10; Length 639;

Db 225 CACGTGTTCTGCGCCGCTGCTGAGATTGACACCACTAGCTGGGCAAGGCTTCTTGCGC 166
QY 2426 ATGATGATAGAACTGTTGCTCTTTCCACCTAAGAGTATCTTGACCTCTTGCGCTGT 2485
Db 165 ATGATGATAGAACTGTTGCTCTTTCCACCTAAGAGTATCTTGACCTCTTGCGCTGT 106
QY 2486 ATGCTTACAAATGCTGATGCTTATGGAAGGCTGTTAAATATATCTTGTTAAAGCA 2545
Db 105 ATGCTTACAAATGCTGATGCTTATGGAAGGCTGTTAAATATATCTTGTTAAAGCA 46
QY 2546 AATTAAGTTGCTCTATTTTGGACATTAACATTAATATATTTT 2590
Db 45 AATTAAGTTGCTCTATTTTGGACATTAACATTAATATATTTT 1
RESULT 9
LOCUS G33851 338 bp DNA linear STS 01-JUL-1997
DEFINITION human STS SHGC-50253, sequence tagged site.
ACCESSION G33851
VERSION G33851.1 GI:2227155
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS Myers,R.M.
JOURNALS Unpublished (1997)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 415/7259687
Fax: 415/7259689
Email: myers@shgc.stanford.edu
Primer A: TTACGGCAATAATGAACTGC
Primer B: TGGTACTGAAATGCGACCA
STS size: 99
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3
Redeveloped chromosome 4 markers for scoring on oligonucleotide arrays. Designed and developed at the Stanford Human Genome Center on sequences previously developed as STS at the Stanford Human Genome Center or the Whitehead Institute.
FEATURES
source
1..338
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="4"
STS
223..321
primer_bind
223..243

primer_bind complement(302..321)
BASE COUNT 101 a 57 c 63 g 114 t 3 others
ORIGIN
Query Match 12.6%; Score 329.2; DB 11; Length 338;
Best Local Similarity 98.2%; Pred. No. 2e-68;
Matches 331; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1129 AATTCCTATTTTGAATTTTCATATATGCTTTTCTGTAAGTTTTCAGAGATTTTAA 1188
Db 2 AATTCCTATTTTGAATTTTTCATATATGCTTTTCTGTAAGTTTTCAGAGATTTTAA 61
QY 1189 AATCAGAAATCATCTAATATGATATTAGCCTATCAAAACTCTCCAAAGCCACACAC 1248
Db 62 AATCAGAAATCATCTAATATGATATTAGCCTATCAAAACTCTCCAAAGCCACACAC 121
QY 1249 CAGTTCCTGACCTCAATTTGAAAGGTTTGTAGACAGAGGAGATTAAGAGTGAGT 1308
Db 122 CAGTTCCTGACCTCAATTTGAAAGGTTTGTAGACAGAGGAGATTAAGAGTGAGT 181
QY 1309 TTAATTAAGCTTAACTAGCTAGGTAAGTAATGAATAATATTACGGCAATTAAGTA 1368
Db 182 TTAATTAAGCTTAACTAGCTAGGTAAGTAATGAATAATATTACGGCAATTAAGTA 241
QY 1369 GCTTCACGCTTTCTGTTGTTGACTTCTCCTACCTAATGTTTAAAGAGCAACAAAGCTTA 1428
Db 242 GCTTCACGCTTTCTGTTGTTGACTTCTCCTACCTAATGTTTAAAGAGCAACAAAGCTTG 301
QY 1429 TGGTCCATTTTCAGTAACACGCGTGTGTTTAGATG 1465
Db 302 TGGTCCATTTTCAGTAACACGCGTGTGTTTAGATG 338
RESULT 10
LOCUS AX198087 470 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 542 from Patent WO0151513.
ACCESSION AX198087
VERSION AX198087.1 GI:15388402
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 470)
AUTHORS Algate,P.A.
TITLE Ovarian tumor-associated sequences
JOURNAL Patent: WO 0151513-A 542 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..470
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/db_xref="taxon:9606"
BASE COUNT 119 a 98 c 96 g 151 t 6 others
ORIGIN
Query Match 11.6%; Score 303.2; DB 6; Length 470;
Best Local Similarity 97.9%; Pred. No. 3.7e-62;
Matches 327; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
QY 1952 CCTGATTTTGTGCTTATTCACACTAAGTAGATCATATCTCTTCTTTTAAAGTTAA 2011
Db 2 CCTGATTTTGTGCTTATTCACACTAAGTAGATCATATCTCTTCTTTTAAAGTTAA 61
QY 2012 TGAGGAATTTAGCTCCACATCAACAAATGTCATTCAGCAAGGCTTCATATCTGCT 2071
Db 62 TGAGGAATTTAGCTCCACATCAACAAATGTCATTCAGCAAGGCTTCATATCTGCT 121
QY 2072 GTGGCTGCTGATAAGAGAGCTTATTCAGATTTCTGCGCTTATTAAGCTTCACTTAC 2131
Db 122 GTGGCTGCTGATAAGAGAGCTTATTCAGATTTCTGCGCTTATTAAGCTTCACTTAC 181
QY 2132 ATGCTGGAAGCTGGCGTGAAGGACAGATGTATTCATCTGCTGTTACTGAAAAACAGTGT 2191

| Db | 182 | ATGCTGGAGACCGGGGTAGGACACAGATGATTCATCTCGNNGTTACTGTAAGAAAAACAGGTCT | 241 |
|-----------------------|--|--|-------------------|
| Qy | 2192 | GATCCTGTTAGTGACTGATCTATTAAGTACCTTAAATGTCACTGTTCAAAATTAGCAAGTCTTC | 2251 |
| Db | 242 | GATCCTGTTAGTGACTGATCTATTAAGTACCTTAAATGTCACTGTTCAAAATTAGCAAGTCTTC | 2299 |
| Qy | 2252 | TAAACAACCTAAACTCTTCAAAATGCTTGGAAAGAT | 2285 |
| Db | 300 | TAAACAACCTAAACTCTTCAAAATGCTTGGAAAGAT | 333 |
| RESULT 11 | | | |
| LOCUS | AX208670 | 470 bp | linear |
| DEFINITION | Sequence 510 from patent WO0157207. | | |
| ACCESSION | AX208670 | | |
| VERSION | AX208670.1 | GI:15423093 | |
| KEYWORDS | | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 470) | | |
| AUTHORS | Algate,P.A. and Mannon,J. | | |
| TITLE | Compositions and methods for the therapy and diagnosis of ovarian cancer | | |
| JOURNAL | Patent: WO 0157207-A 510 09-AUG-2001; | | |
| FEATURES | CORIXA CORPORATION (US) | | |
| SOURCE | location/qualifiers | | |
| | 1..470 | | |
| | /organism="Homo sapiens" | | |
| | /db_xref="taxon:9606" | | |
| BASE COUNT | 119 a 98 c 96 g 151 t | 6 others | |
| ORIGIN | | | |
| Query Match | 11.6%; | Score 303.2; | DB 6; Length 470; |
| Best Local Similarity | 97.9%; | Pred. No. 3.7e-62; | |
| Matches 327; | Conservative 0; | Mismatches 5; | Indels 2; |
| | | | Gaps 2. |
| Qy | 1952 | CCTGATTTTTTGTCTTATTCACAAGTATGATCATATTCCTTCTCTTTATGTTAA | 2011 |
| Db | 2 | CCTGATTTTTTGTCTTATTCACAAGTATGATCATATTCCTTCTCTTTATGTTAA | 61 |
| Qy | 2012 | TGAGAGATTATTAAGCCTCCACATCAACAATGTTCAATTCCAGACGGCTTTCATCTCTGCT | 2071 |
| Db | 62 | TGAGAGATTATTAAGCCTCCACATCAACAATGTTCAATTCCAGACGGCTTTCATCTCTGCT | 121 |
| Qy | 2072 | GTGGATCGTGTGATAAGAGACTTATTCAGGTTTCTCGCCTTACCTATTAAGCTCCACTTCAC | 2131 |
| Db | 122 | GTGGATCGTGTGATAAGAGACTTATTCAGGTTTCTCGCCTTACCTATTAAGCTCCACTTCAC | 181 |
| Qy | 2132 | ATGCTGGAGACTGGCGGTAGGGACAGATGATTCATCTCGTGTCTACTGTAAGAAACAGGTCT | 2191 |
| Db | 182 | ATGCTGGAGACTGGCGGTAGGGACAGATGATTCATCTCGTGTGTACTGTAAGAAACAGGTCT | 241 |
| Qy | 2192 | GATCCTGTTAGTGACTGATCTATTAAGTACCTTAAATGTCACTGTTCAAAATTAGCAAGTCTTC | 2251 |
| Db | 242 | GATCCTGTTAGTGACTGATCTATTAAGTACCTTAAATGTCACTGTTCAAAATTAGCAAGTCTTC | 2299 |
| Qy | 2252 | TAAACAACCTAAACTCTTCAAAATGCTTGGAAAGAT | 2285 |
| Db | 300 | TAAACAACCTAAACTCTTCAAAATGCTTGGAAAGAT | 333 |
| RESULT 12 | | | |
| LOCUS | G21512/c | 425 bp | DNA linear |
| DEFINITION | human STS WI-14698, sequence tagged site. | | |
| ACCESSION | G21512 | | |
| VERSION | G21512.1 | GI:1341838 | |
| KEYWORDS | STS: STS sequence; primer: sequence tagged site. | | |
| SOURCE | human STS derived from sequences in dbEST and the UniGene | | |

| ORGANISM | collection. |
|---|---|
| Homo sapiens | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | |
| REFERENCE | 1 (bases 1 to 425) |
| AUTHORS | Hudson,T. |
| TITLE | Whitehead Institute/MIT Center for Genome Research; Physically |
| JOURNAL | Mapped STS |
| COMMENT | Unpublished |
| | Contact: Thomas Hudson |
| | Whitehead Institute/MIT Center for Genome Research |
| | Whitehead Institute for Biomedical Research |
| | 9 Cambridge Center, Cambridge MA 02142 USA |
| | Tel: 617 252 1900 |
| | Fax: 617 252 1902 |
| | Email: thudson@genome.wi.mit.edu |
| | Primer A: CAACCTTAATTTCCCTTAACAGGA |
| | Primer B: GATGTAGACTGTGTCCTTTCC |
| | STS size: 129 |
| | PCR Profile: |
| | Presoak: |
| | Denaturation: |
| | Annealing: 56 degrees C |
| | Polymerization: |
| | PCR Cycles: 35 |
| | Thermal Cycler: |
| | Protocol: |
| | Template: 10 ng |
| | Primer: each 5 pM |
| | dNTPs: each 4 mM |
| | Tag Polymerase: 0.025 units/ul |
| | Total Vol: 20 ul |
| | Buffer: |
| | MgCl2: 1.5 mM |
| | KCl: 50 mM |
| | Tris-HCL: 10 mM |
| | pH: 9.3 |
| FEATURES | Derived from dbEST (genbank accession H15695). |
| source | Location/Qualifiers |
| | 1..425 |
| | /organism="Homo sapiens" |
| | /db_xref="taxon:9606" |
| | /map="532.1 kb from top of Chr4 linkage group" |
| STS | 16..144 |
| primer_bind | 16..40 |
| primer_bind | complement(120..144) |
| BASE COUNT | 135 a 84 c 87 g 112 t 7 others |
| ORIGIN | |
| Query Match | 8.5%; Score 221; DB 11; Length 425; |
| Best Local Similarity | 90.7%; Pred. No. 2.1e-42; |
| Matches 302; Conservative | 0; Mismatches 22; Indels 9; Gaps 6; |
| OY | 2249 TTCTAACAACAAACTGCTGCTTCAAAAGCCCAATCTTTA 2304 |
| Db | 333 TCCTACCAACAACTCTTAAATGCTTGGAAGATACCTACAAAGCCCAATCTTTA 274 |
| OY | 2305 TAGAATTTGGGCC--AAGATTAATCTATGTTGTTTGCAATG-GCTATTGTTAAGCTCCANA 2361 |
| Db | 273 TAGAATTTGGGCCCAAGATTAATGCAATGTTGTTTGCAATGCTAATGTTAAGCTCCANA 214 |
| OY | 2362 GGTTCACGTGTGTTT-CTGCCGCTG-TCTGGAAGTTGTCAACACGTGAGGGCAAGGCTTC 2419 |
| Db | 213 GGTTCACGTGTGTTTCTGCGCGCTGNNCCGGAGTTGTCTACCACTGGGCAAGGCTTC 154 |
| OY | 2420 TTGGGCATGATGTGAACCTGTTGTCCTTTTCCCACTAACATGTAATCTTTGAAGCTGCTTG 2479 |
| Db | 153 TTGGGCATGATGTGAACCTGTTGTCCTTTTCCCACTAACATGTAATCTTTGAAGCTGCTTG 94 |

| | | | |
|--|---|---|-----------------|
| OY | 2480 | CCGTGTATGCTTACCAAAATGCGATGGCCCTTTATGAGAGCCTGTTAAATTAATTCCTGTT | 2539 |
| Db | 93 | CCTGTATGCTTACCAAAATGCGATGGCCCTTTATGAGAGCCTGTTAAATTAATTCCTGTT | 34 |
| OY | 2540 | AAAGGAATTAAGTTTGCTATTTTTGACAAAT | 2572 |
| Db | 33 | AAAGGAATTAAGTTTGCTATTTTTGACAAAT | 1 |
| RESULT 13 | | | |
| LOCUS | G33614 | 425 bp | DNA |
| DEFINITION | human STS SHGC-50534, sequence tagged site. | linear | STS 01-JUL-1997 |
| ACCESSION | G33614 | | |
| VERSION | G33614.1 | GI:2226918 | |
| KEYWORDS | STS, STS sequence, primer, sequence tagged site. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| JOURNAL | 1 (bases 1 to 425) | | |
| COMMENT | Myers, R.M. | | |
| | Unpublished (1997) | | |
| | Contact: Richard M. Myers | | |
| | Stanford Human Genome Center (SHGC) | | |
| | Stanford University School of Medicine | | |
| | Department of Genetics, M-344, Stanford, CA 94305, USA | | |
| | Tel: 4157259689 | | |
| | Fax: 4157259689 | | |
| | Email: myerseshgc.stanford.edu | | |
| | Primer A: TAATTTACAGCCCTTCATTAAGCC | | |
| | Primer B: ACAACTAACTCCTTCAATGCC | | |
| | STS size: 284 | | |
| | PCR Profile: | | |
| | Initial incubation: 94 degrees C for 90 seconds | | |
| | Denaturation: 94 degrees C for 15 seconds | | |
| | Annealing: 62 degrees C for 23 seconds | | |
| | Polymerization: 72 degrees C for 30 seconds | | |
| | PCR Cycles: 30 | | |
| | Thermal Cycler: Perkin Elmer 9600 | | |
| | Protocol: | | |
| | Template: 25 ng | | |
| | Primer: each 1 uM | | |
| | dNTPs: each 200 uM | | |
| | Tag Polymerase: 0.05 units/uL | | |
| | Total Vol: 10 uL | | |
| | Buffer: | | |
| | MgCl2: 2.5 mM | | |
| | KCl: 50 mM | | |
| | Tris-HCl: 20 mM | | |
| | pH: 8.3 | | |
| Redeveloped chromosome 4 markers for scoring on oligonucleotide arrays. Designed and developed at the Stanford Human Genome Center on sequences previously developed as STSs at the Stanford Human Genome Center or the Whitehead Institute. | | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..425 | | |
| | /organism="Homo sapiens" | | |
| | /db_xref="taxon:9606" | | |
| | /map="4" | | |
| STS | 45..328 | | |
| primer_bind | 45..68 | | |
| primer_bind | complement(305..328) | | |
| BASE COUNT | 135 a 84 c 87 g 112 t 7 others | | |
| ORIGIN | | | |
| Query Match | 8.5%; Score 221; DB 11; Length 425; | | |
| Best Local Similarity | 90.7%; Pred.No. 2.1e-42; | | |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------------------|---|--|--------------------|------------|--------------|--|-----------------|------|------|---|------|----|-----|--|-----|----|------|--|------|----|-----|---|-----|----|------|--|------|----|-----|---|-----|----|------|--|------|----|----|--|----|----|------|--------------------------------|------|----|----|--------------------------------|---|
| Matches | 302; | Conservative | 0; | Mismatches | 22; | Indels | 9; | Gaps | 6; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OY | 2249 | TTCTACAAACTAANACTC--TTCNAATGCTTGGAAGAAGATAC--TGCNAAAACCATACTTTTA | 2304 | Dd | 333 | TCTCAACAACACTAACTCCCTTCMAATGGCTGTGGAAAGATTACCTAACAAAGCCCACCTTTTA | 274 | OY | 2305 | TAGAATTGGGCC--TAGATFAAATCTATGTTGTTTTGCATCG--CCATTGTGTAAGCTCCAAA | 2361 | Dd | 273 | TAGATTTGGGCCCCAAGATRAATATGCAATATGTTGTTTGGCATGTMCTATTTGTTAAGCTCCAAA | 214 | OY | 2362 | GGTTCACGTGTGTTT-CTGCCGCTG-TCCGTGAGTTGTGCACACACTGACGTGGGCAAGGCTTC | 2419 | Dd | 213 | GGTTCACGTGTGTTTNCGTCCCGCTGNMCCGTGGAGTGTGCACCACTGACTGGGCAAGGCTTC | 154 | OY | 2420 | TTGGGCATGAGATGTGANAAGCTGTGTTCCTTTTCCCACCTAACATTTATCTTTGACTCTCTTG | 2479 | Dd | 153 | TTGGGCATCGATGTATGAAGCTGTGTTCCTTTTCCACTAACATTTATCTTTGACTCTCTTG | 94 | OY | 2480 | CCTGTATGCTTACCAAATGGTGAATGGCTTATGAGAAGCGTGTAAATTAATATTCCTGTT | 2539 | Dd | 93 | CCTGTATGCTTACCAAATGGTGAATGGCTTATGAGAAGCGTGTAAATTAATATTCCTGTT | 34 | OY | 2540 | AAAGGAATTAAGTTTGCTATTTTGTACANT | 2572 | Dd | 33 | AAAGGAATTAAGTTTGCTATTTTGTACANT | 1 |
| RESULT 14 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| LOCUS | AXO15378 | | 1491 bp | DNA | | Linear | PAT 07-SEP-2000 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DEFINITION | Sequence 40 from Patent WO9951727. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ACCESSION | AXO15378 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| VERSION | AXO15378.1 | GI:10041358 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| KEYWORDS | human. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SOURCE | ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. SCMITT,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C. Human nucleic acid sequences of normal ovary tissue Patent: WO 9951727-A 40 14-OCT-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| FEATURES | source location/qualifiers 1..1491 /organism="Homo sapiens" /db_xref="taxon:9606" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| BASE COUNT | 323 a | 362 c | 455 g | 351 t | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ORIGIN | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Query Match | 2.6%: | | Score 67.2: | DB 6: | Length 1491: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Best Local Similarity | 51.2%: | | Pred. No. 2.3e-05: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Matches | 206; | Conservative | 0; | Mismatches | 193; | Indels | 3; | Gaps | 2; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OY | 351 | GAGGAATCAACTGCGCACATTTGGTTAAAAAGTGGGAAACTGTCTGTCCAAATCAANG | 410 | Dd | 194 | GATGACACATTGTGTGCGCAACTGATGACAGCTGCTGACGAGAAAGCCCGCCACGCGCG | 253 | OY | 411 | CAAACTAAACTTGTGTGTCNAAGAGTCTGTGCCGTGAGAAAATGACGACGAGAAATTTGCT | 470 | Dd | 254 | CTGGGCTCTCGACGCGCTCGCGGCTGCTGATGATGCTTACGCACTGTATGACCAAGTGGG | 313 | OY | 471 | CAAGATGTCCTGCGGCTTTTCTCAACGAGAGCCCTGCGGCTTCCGAGAGTTGTGTATGCAC | 530 | Dd | 314 | AAGAGAACTACGCGCTCGGCTTACGACGACGCGCTGCGGCTTCGGGGGCGCTGCTGGAC | 373 | OY | 531 | GTGAACTTGGAAATTTGAANAATGTATGTATAAAAGCTGATGATTTGTGTGATTCTTAC | 590 | Dd | 374 | GTCTCGTGTGAGACGACGACGAGAGCTGCGCACACGCTGTGGGCGGCACTGGCACTGACCCAC | 433 | | | | | | | | | | | | | | | | |

| | | | | |
|-----------------------|--------|--------------------|-------|--------------|
| Query Match | 2.68; | Score 67.2; | DB 9; | Length 1732; |
| Best Local Similarity | 51.28; | Pred. No. 2.4e-05; | | |

Search completed: October 13, 2002, 03:03:37
Job time : 4759 secs

